

TRANSMITTAL LETTER TO THE UNITED STATES

DESIGNATED/ELECTED OFFICE (DO/EO/US)

CONCERNING A FILING UNDER 35 U.S.C. 371

CGAB-210 USA

U.S. APPLICATION NO. (IF KNOWN, SEE 37 CFR

09/367013

INTERNATIONAL APPLICATION NO.
PCT/US98/07126INTERNATIONAL FILING DATE
10 April 1998 (10.04.98)PRIORITY DATE CLAIMED
11 April 1997 (11.04.97)

TITLE OF INVENTION

METHODS AND COMPOSITIONS FOR SYNTHESIS OF LONG CHAIN POLYUNSATURATED FATTY ACIDS

APPLICANT(S) FOR DO/EO/US

KNUTZON, Deborah; MUKERJI, Pradip; HUANG, Yung-Sheng; THURMOND, Jennifer; CHAUDHARY, Sunita;
and LEONARD, Amanda Eun-Yeong

Applicant herewith submits to the United States Designated/Elected Office (DO/EO/US) the following items and other information:

1. ☒ This is a **FIRST** submission of items concerning a filing under 35 U.S.C. 371.
2. ☐ This is a **SECOND** or **SUBSEQUENT** submission of items concerning a filing under 35 U.S.C. 371.
3. ☒ This is an express request to begin national examination procedures (35 U.S.C. 371(f)) at any time rather than delay examination until the expiration of the applicable time limit set in 35 U.S.C. 371(b) and PCT Articles 22 and 39(1).
4. ☒ A proper Demand for International Preliminary Examination was made by the 19th month from the earliest claimed priority date.
5. ☒ A copy of the International Application as filed (35 U.S.C. 371 (c) (2))
 - a. ☒ is transmitted herewith (required only if not transmitted by the International Bureau).
 - b. ☐ has been transmitted by the International Bureau.
 - c. ☐ is not required, as the application was filed in the United States Receiving Office (RO/US).
6. ☐ A translation of the International Application into English (35 U.S.C. 371(c)(2)).
7. ☒ A copy of the International Search Report (PCT/ISA/210).
8. ☒ Amendments to the claims of the International Application under PCT Article 19 (35 U.S.C. 371 (c)(3))
 - a. ☐ are transmitted herewith (required only if not transmitted by the International Bureau).
 - b. ☐ have been transmitted by the International Bureau.
 - c. ☐ have not been made; however, the time limit for making such amendments has NOT expired.
 - d. ☒ have not been made and will not be made.
9. ☐ A translation of the amendments to the claims under PCT Article 19 (35 U.S.C. 371(c)(3)).
10. ☒ An oath or declaration of the inventor(s) (35 U.S.C. 371 (c)(4)). (three signed documents)
11. ☒ A copy of the International Preliminary Examination Report (PCT/IPEA/409).
12. ☐ A translation of the annexes to the International Preliminary Examination Report under PCT Article 36 (35 U.S.C. 371 (c)(5)).

Items 13 to 18 below concern document(s) or information included:

13. ☐ An Information Disclosure Statement under 37 CFR 1.97 and 1.98.
14. ☒ An assignment document for recording. A separate cover sheet in compliance with 37 CFR 3.28 and 3.31 is included.
15. ☒ A **FIRST** preliminary amendment.
A **SECOND** or **SUBSEQUENT** preliminary amendment.
16. ☐ A substitute specification.
17. ☐ A change of power of attorney and/or address letter.
18. ☒ Certificate of Mailing by Express Mail
19. ☒ Other items or information:

- a. Twenty (20) sheets of formal drawings.
- b. Copies of Forms PCT/IB/301, PCT/IB/304, PCT/IB/308, and PCT/IB/332.
- c. Copy of Response to Invitation to Furnish Nucleotide and/or Amino Acid Sequence Listing with revised paper copy of Sequence Listing (pages 143-173) and revised copy of Sequence Listing in computer readable format.

U.S. APPLICATION NO. 09/367013 (SEE 37 CFR 1.53)	INTERNATIONAL APPLICATION NO. PCT/US98/07126	ATTORNEY'S DOCKET NUMBER CGAB-210 USA
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20. The following fees are submitted: BASIC NATIONAL FEE (37 CFR 1.492 (a) (1) - (5)) : <input type="checkbox"/> Search Report has been prepared by the EPO or JPO \$840.00 <input type="checkbox"/> International preliminary examination fee paid to USPTO (37 CFR 1.482) \$670.00 <input type="checkbox"/> No international preliminary examination fee paid to USPTO (37 CFR 1.482) but international search fee paid to USPTO (37 CFR 1.445(a)(2)) \$760.00 <input checked="" type="checkbox"/> Neither international preliminary examination fee (37 CFR 1.482) nor international search fee (37 CFR 1.445(a)(2)) paid to USPTO \$970.00 <input type="checkbox"/> International preliminary examination fee paid to USPTO (37 CFR 1.482) and all claims satisfied provisions of PCT Article 33(2)-(4) \$96.00	<table border="1" style="width:100%; border-collapse: collapse;"> <tr> <th colspan="2" style="text-align: left;">CALCULATIONS PTO USE ONLY</th> </tr> <tr> <td style="width:50%;"></td> <td style="width:50%;"></td> </tr> </table>	CALCULATIONS PTO USE ONLY			
CALCULATIONS PTO USE ONLY					

ENTER APPROPRIATE BASIC FEE AMOUNT =	\$970.00
Surcharge of \$130.00 for furnishing the oath or declaration later than <input type="checkbox"/> 20 <input type="checkbox"/> 30 months from the earliest claimed priority date (37 CFR 1.492 (e)).	\$0.00

CLAIMS	NUMBER FILED	NUMBER EXTRA	RATE		
Total claims	124 - 20 =	104	x \$18.00		\$1,872.00
Independent claims	11 - 3 =	8	x \$78.00		\$624.00
Multiple Dependent Claims (check if applicable). <input type="checkbox"/>					\$0.00

TOTAL OF ABOVE CALCULATIONS =	\$3,466.00
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Reduction of 1/2 for filing by small entity, if applicable. Verified Small Entity Statement must also be filed (Note 37 CFR 1.9, 1.27, 1.28) (check if applicable). <input type="checkbox"/>	\$0.00
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SUBTOTAL =	\$3,466.00
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Processing fee of \$130.00 for furnishing the English translation later than <input type="checkbox"/> 20 <input type="checkbox"/> 30 months from the earliest claimed priority date (37 CFR 1.492 (f)).	\$0.00
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TOTAL NATIONAL FEE =	\$3,466.00
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Fee for recording the enclosed assignment (37 CFR 1.21(h)). The assignment must be accompanied by an appropriate cover sheet (37 CFR 3.28, 3.31) (check if applicable). <input checked="" type="checkbox"/>	\$40.00
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TOTAL FEES ENCLOSED =	\$3,506.00
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	Amount to be refunded	\$
	charged	\$

☒ A check in the amount of **\$3,506.00** to cover the above fees is enclosed.

☐ Please charge my Deposit Account No. _____ in the amount of _____ to cover the above fees.
 A duplicate copy of this sheet is enclosed.

☒ The Commissioner is hereby authorized to charge any fees which may be required, or credit any overpayment to Deposit Account No. **12-1420** A duplicate copy of this sheet is enclosed.

NOTE: Where an appropriate time limit under 37 CFR 1.494 or 1.495 has not been met, a petition to revive (37 CFR 1.137(a) or (b)) must be filed and granted to restore the application to pending status.

SEND ALL CORRESPONDENCE TO:

Michael R. Ward, Esq.
 LIMBACH & LIMBACH L.L.P.
 2001 Ferry Building
 San Francisco, California 94111-4262
 Telephone: (415) 433-4150

Michael R. Ward
 SIGNATURE

Michael R. Ward
 NAME

38,651
 REGISTRATION NUMBER

August 5, 1999
 DATE

PATENT

PATENT COOPERATION TREATY
UNITED STATES DESIGNATED/ELECTED OFFICE (DO/EO/US)

In re Nat'l Phase Application of:)
DEBORAH KNUTZON et al.)
Based Upon International) CERTIFICATION
Application No. PCT/US98/07126) UNDER
Int'l Filing Date: April 10, 1998) 37 CFR §1.10
Serial No.: Not Assigned)
A Filing Under 35 U.S.C. 371 on:)
August 5, 1999)
For: **METHODS AND COMPOSITIONS FOR**)
SYNTHESIS OF LONG CHAIN)
POLYUNSATURATED FATTY ACIDS)
_____)

Assistant Commissioner for Patents
Box PCT
Washington, D.C. 20231-0001

Attention: U.S. Designated/Elected Office (DO/EO/US)

Dear Sir:

I hereby certify that this Application for entering the national phase of the above-identified International Application and the documents referred to as enclosed herein are being deposited with the United States Postal Service on this date, **August 5, 1999**, in an envelope bearing "Express Mail Post Office to Addressee" Mailing Label Number **EM461821031US** addressed to: Assistant Commissioner for Patents, Box PCT, Washington, D.C. 20231-0001, Attention U.S. Designated/Elected Office (DO/EO/US).

Enclosed are:

1. Transmittal Letter to the U.S. Designated/Elected Office (DO/EO/US) Concerning A Filing Under 35 U.S.C. 371, in duplicate;
2. Copy of Request, description, sequence listing, claims, abstract, and drawings of International Application No. PCT/US98/07126 as originally filed April 10, 1998;

3. Twenty (20) sheets of formal drawings, comprising Figures 1 through 10B, inclusive;
4. International Search Report;
5. Response to Invitation to Furnish Nucleotide and/or Amino Acid Sequence Listing with revised paper copy of Sequence Listing (pages 143-173) and revised copy of Sequence Listing in computer readable format;
6. International Preliminary Examination Report;
7. Forms PCT/IB/301, PCT/IB/304, PCT/IB/308, and PCT/IB/332;
8. Preliminary Amendment;
9. Combined Declaration/Power of Attorney/Claim of Priority (**three signed documents**);
10. Assignment with Recordation Form PTO-1595;
11. Check in the amount of \$3,506.00; and
12. Acknowledgement Postcard.

Dated: August 5, 1999


Elizabeth A. Reicker

LIMBACH & LIMBACH L.L.P.
2001 Ferry Building
San Francisco, California 94111
Telephone: (415) 433-4150

Attorney Docket No. CGAB-210 USA

PATENT
09/367013
514 Rec'd PCT/PTO 05 AUG 1999

IN THE UNITED STATES PATENT AND TRADEMARK OFFICE

In re application of: Deborah Knutzon, et al.)	Group Art Unit:
Serial No.: To Be Determined)	Examiner:
Filed: Herewith)	PRELIMINARY AMENDMENT
For: METHODS AND COMPOSITIONS)	2001 Ferry Building
FOR SYNTHESIS OF LONG CHAIN)	San Francisco, CA 94111
POLY-UNSATURATED FATTY ACIDS)	Attorney Docket: CGAB-210 USA

Assistant Commission for Patents
Washington, D.C. 20231

Sir:

Prior to examination of the above-referenced patent application, please enter the following amendments and remarks.

In the Claims

Cancel claims 1-64.

65. (Amended) A method for obtaining altered long chain polyunsaturated fatty acid biosynthesis comprising the steps of:

growing [a plant having] microbial cells which contain one or more transgenes[, derived from a fungus or algae,] which encodes a transgene expression product [which desaturates a fatty acid molecule at a carbon selected from the group consisting of carbon 6 and carbon 12 from the carboxyl end of said fatty acid molecule wherein said one or more transgenes is operably associated with an expression control sequence,] under conditions whereby said one or more transgenes is expressed, whereby long chain polyunsaturated fatty acid biosynthesis in said cells is altered whereby said transgene comprises a nucleotide sequence which encodes a polypeptide wherein the sequence of the polypeptide comprises a sequence selected from the group consisting of residues 50-53, 39-43, 172-176, 204-213 and 390-402 of SEQ ID NO:2.

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66. (Amended) The method according to claim 65, wherein said long chain polyunsaturated fatty acid is selected from the group consisting of [18:1 ω 9, LA, GLA, SDA and ALA] oleic acid, linolenic acid, gamma-linolenic acid, stearidonic acid and alpha-linolenic acid.

67. (Reiterated) A microbial oil or fraction thereof produced according to the method of claim 65.

68. (Reiterated) A method of treating or preventing malnutrition comprising administering said microbial oil of claim 67 to a patient in need of said treatment or prevention in an amount sufficient to effect said treatment or prevention.

69. (Amended) A pharmaceutical composition comprising said microbial oil or fraction thereof of claim 67 and a pharmaceutically acceptable carrier.

70. (Reiterated) The pharmaceutical composition of claim 69, wherein said pharmaceutical composition is in the form of a solid or a liquid.

71. (Reiterated) The pharmaceutical composition of claim 70, wherein said pharmaceutical composition is in a capsule or tablet form.

72. (Reiterated) The pharmaceutical composition of claim 69 further comprising at least one nutrient selected from the group consisting of a vitamin, a mineral, a carbohydrate, a sugar, an amino acid, a free fatty acid, a phospholipid, an antioxidant, and a phenolic compound.

73. (Reiterated) A nutritional formula comprising said microbial oil or fraction thereof of claim 67.

74. (Reiterated) The nutritional formula of claim 73, wherein said nutritional formula is selected from the group consisting of an infant formula, a dietary supplement, and a dietary substitute.

75. (Reiterated) The nutritional formula of claim 74, wherein said infant formula, dietary supplement or dietary supplement is in the form of a liquid or a solid.

76. (Reiterated) An infant formula comprising said microbial oil or fraction thereof of claim 67.

77. (Reiterated) The infant formula of claim 76 further comprising at least one macronutrient selected from the group consisting of coconut oil, soy oil, canola oil, mono- and diglycerides, glucose, edible lactose, electrodialysed whey, electrodialysed skim milk, milk whey, soy protein, and other protein hydrolysates.

78. (Reiterated) The infant formula of claim 77 further comprising at least one vitamin selected from the group consisting of Vitamins A, C, D, E, and B complex; and at least one mineral selected from the group consisting of calcium, magnesium, zinc, manganese, sodium, potassium, phosphorus, copper, chloride, iodine, selenium, and iron.

79. (Reiterated) A dietary supplement comprising said microbial oil or fraction thereof of claim 67.

80. (Reiterated) The dietary supplement of claim 79 further comprising at least one macronutrient selected from the group consisting of coconut oil, soy oil, canola oil, mono- and diglycerides, glucose, edible lactose, electrodialysed whey, electrodialysed skim milk, milk whey, soy protein, and other protein hydrolysates.

81. (Reiterated) The dietary supplement of claim 80 further comprising at least one vitamin selected from the group consisting of Vitamins A, C, D, E, and B complex; and at least one mineral selected from the group consisting of calcium, magnesium, zinc, manganese, sodium, potassium, phosphorus, copper, chloride, iodine, selenium, and iron.

82. (Amended) The dietary supplement of claim 79 [or claim 81,] wherein said dietary supplement is administered to a human or an animal.

83. (Reiterated) A dietary substitute comprising said microbial oil or fraction thereof of claim 67.

84. (Reiterated) The dietary substitute of claim 83 further comprising at least one macronutrient selected from the group consisting of coconut oil, soy oil, canola oil, mono- and diglycerides, glucose, edible lactose, electrodialysed whey, electrodialysed skim milk, milk whey, soy protein, and other protein hydrolysates.

85. (Reiterated) The dietary substitute of claim 84 further comprising at least one vitamin selected from the group consisting of Vitamins A, C, D, E, and B complex; and at least one mineral selected from the group consisting of calcium, magnesium, zinc, manganese, sodium, potassium, phosphorus, copper, chloride, iodine, selenium, and iron.

86. (Amended) The dietary substitute of claim 83 [or claim 85,] wherein said dietary substitute is administered to a human or animal.

87. (Amended) A method of treating a patient having a condition caused by insufficient intake or production of polyunsaturated fatty acids comprising administering to said patient [said dietary substitute of claim 83 or]

said dietary supplement of claim 79 in an amount sufficient to effect said treatment.

88. (Amended) The method of claim 87, wherein [said dietary substitute or] said dietary supplement is administered enterally or parenterally.

89. (Reiterated) A cosmetic comprising said microbial oil or fraction thereof of claim 67.

90. (Reiterated) The cosmetic of claim 88, wherein said cosmetic is applied topically.

91. (Reiterated) The pharmaceutical composition of claim 69, wherein said pharmaceutical composition is administered to a human or an animal.

92. (Reiterated) An animal feed comprising said microbial oil or fraction thereof of claim 67.

93. (Amended) The method of claim [20] 65 wherein said microbial cells are [fungus is Mortierella species] fungal cells.

94. (Amended) The method of claim 93 wherein said [fungus is] fungal cells are [Mortierella alpina.] yeast cells.

95. (Amended) An isolated polypeptide wherein said polypeptide has a peptide sequence selected from the group consisting of SEQ ID NO:34 - SEQ ID NO:40.

96. (Amended) An isolated polypeptide wherein said polypeptide has a peptide sequence selected from the group consisting of SEQ ID NO:20, SEQ ID NO:22, SEQ ID NO:25 and SEQ ID NO:26.

97. (Reiterated) A method for production of gamma-linolenic acid in a eukaryotic cell culture, said method comprising:

growing a eukaryotic cell culture having a plurality of recombinant eukaryotic cells, wherein said recombinant eukaryotic cells or ancestors of said recombinant eukaryotic cells were transformed with a vector comprising fungal DNA encoding a polypeptide which converts linoleic acid to gamma-linolenic acid, wherein said DNA is operably associated with an expression control sequence functional in said recombinant eukaryotic cells, under conditions whereby said DNA is expressed, whereby gamma-linolenic acid is produced from linoleic acid in said eukaryotic cell culture.

98. (Amended) The method according to Claim 97 wherein said eukaryotic cells are selected from the group consisting of mammalian cells, [plant cells,] fungal cells, avian cells and algal cells.

Insert the following new claims:

--99. A method for producing an oil or fraction thereof comprising growing one or more transgenic microbial cells under suitable conditions whereby said cells express a transgenic polypeptide wherein the sequence of said polypeptide comprises a sequence selected from the group consisting of residues 50-53, 39-43, 172-176, 204-213 and 390-402 of SEQ ID NO:2.

100. A microbial oil or fraction thereof produced according to the method of claim 99.

101. A method of treating or preventing malnutrition comprising administering said microbial oil of claim 100 to a patient in need of said treatment or prevention in an amount sufficient to effect said treatment or prevention.

102. A pharmaceutical composition comprising said microbial oil or fraction of claim 100 and a pharmaceutically acceptable carrier.

103. The pharmaceutical composition of claim 102, wherein said pharmaceutical composition is in the form of a solid or a liquid.

104. The pharmaceutical composition of claim 102, wherein said pharmaceutical composition is in a capsule or tablet form.

105. The pharmaceutical composition of claim 103 further comprising at least one nutrient selected from the group consisting of a vitamin, a mineral, a carbohydrate, a sugar, an amino acid, a free fatty acid, a phospholipid, an antioxidant, and a phenolic compound.

106. A nutritional formula comprising said microbial oil or fraction thereof of claim 100.

107. The nutritional formula of claim 106, wherein said nutritional formula is selected from the group consisting of an infant formula, a dietary supplement, and a dietary substitute.

108. The nutritional formula of claim 107, wherein said infant formula, dietary supplement or dietary supplement is in the form of a liquid or a solid.

109. An infant formula comprising said microbial oil or fraction thereof of claim 100.

110. The infant formula of claim 109 further comprising at least one macronutrient selected from the group consisting of coconut oil, soy oil, canola oil, mono- and diglycerides, glucose, edible lactose, electrodialysed whey, electrodialysed skim milk, milk whey, soy protein, and other protein hydrolysates.

111. The infant formula of claim 110 further comprising at least one vitamin selected from the group consisting of Vitamins A, C, D, E, and B complex; and at least one mineral selected from the group consisting of calcium, magnesium, zinc, manganese, sodium, potassium, phosphorus, copper, chloride, iodine, selenium, and iron.

112. A dietary supplement comprising said microbial oil or fraction thereof of claim 100.

113. The dietary supplement of claim 112 further comprising at least one macronutrient selected from the group consisting of coconut oil, soy oil, canola oil, mono- and diglycerides, glucose, edible lactose, electrodialysed whey, electrodialysed skim milk, milk whey, soy protein, and other protein hydrolysates.

114. The dietary supplement of claim 113 further comprising at least one vitamin selected from the group consisting of Vitamins A, C, D, E, and B complex; and at least one mineral selected from the group consisting of calcium, magnesium, zinc, manganese, sodium, potassium, phosphorus, copper, chloride, iodine, selenium, and iron.

115. The dietary supplement of claim 112 wherein said dietary supplement is administered to a human or an animal.

116. A dietary substitute comprising said microbial oil or fraction thereof of claim 100.

117. The dietary substitute of claim 116 further comprising at least one macronutrient selected from the group consisting of coconut oil, soy oil, canola oil, mono- and diglycerides, glucose, edible lactose, electrodialysed whey, electrodialysed skim milk, milk whey, soy protein, and other protein hydrolysates.

118. The dietary substitute of claim 117 further comprising at least one vitamin selected from the group consisting of Vitamins A, C, D, E, and B complex; and at least one mineral selected from the group consisting of calcium, magnesium, zinc, manganese, sodium, potassium, phosphorus, copper, chloride, iodine, selenium, and iron.

119. The dietary substitute of claim 116 wherein said dietary substitute is administered to a human or animal.

120. A method of treating a patient having a condition caused by insufficient intake or production of polyunsaturated fatty acids comprising administering to said patient said dietary supplement of claim 112 in an amount sufficient to effect said treatment.

121. The method of claim 120, wherein said dietary supplement is administered enterally or parenterally.

122. A method of treating a patient having a condition caused by insufficient intake or production of polyunsaturated fatty acids comprising administering to said patient said dietary substitute of claim 116.

123. The method of claim 122, wherein said dietary substitute is administered enterally or parenterally

124. A cosmetic comprising said microbial oil or fraction thereof of claim 100.

125. The cosmetic of claim 124, wherein said cosmetic is applied topically.

126. The pharmaceutical composition of claim 102, wherein said pharmaceutical composition is administered to a human or an animal.

127. An animal feed comprising said microbial oil or fraction thereof of claim 100.

128. A method for producing an oil or fraction thereof comprising the steps of: growing microbial cells which contain one or more transgenes which encode a transgene expression product under conditions whereby said one or more transgenes are expressed, whereby long chain polyunsaturated fatty acid biosynthesis in said cells is altered whereby said transgene comprises a nucleotide sequence which encodes a polypeptide wherein the sequence of the polypeptide comprises a sequence selected from the group consisting of SEQ ID NO:4, SEQ ID NO:20, SEQ ID NO:22, SEQ ID NO:24 and SEQ ID NO:26.

129. A microbial oil or fraction thereof produced according to the method of claim 128.

130. A method of treating or preventing malnutrition comprising administering said microbial oil of claim 129 to a patient in need of said treatment or prevention in an amount sufficient to effect said treatment or prevention.

131. A pharmaceutical composition comprising said microbial oil or fraction of claim 129 and a pharmaceutically acceptable carrier.

132. The pharmaceutical composition of claim 131 wherein said pharmaceutical composition is in the form of a solid or a liquid.

133. The pharmaceutical composition of claim 131 wherein said pharmaceutical composition is in a capsule or tablet form.

134. The pharmaceutical composition of claim 133 further comprising at least one nutrient selected from the group consisting of a vitamin, a mineral, a carbohydrate, a sugar, an amino acid, a free fatty acid, a phospholipid, an antioxidant, and a phenolic compound.

135. A nutritional formula comprising said microbial oil or fraction thereof of claim 129.

136. The nutritional formula of claim 135 wherein said nutritional formula is selected from the group consisting of an infant formula, a dietary supplement, and a dietary substitute.

137. The nutritional formula of claim 136 wherein said infant formula, dietary supplement or dietary supplement is in the form of a liquid or a solid.

138. An infant formula comprising said microbial oil or fraction thereof of claim 129.

139. The infant formula of claim 138 further comprising at least one macronutrient selected from the group consisting of coconut oil, soy oil, canola

oil, mono- and diglycerides, glucose, edible lactose, electro dialysed whey, electro dialysed skim milk, milk whey, soy protein, and other protein hydrolysates.

140. The infant formula of claim 139 further comprising at least one vitamin selected from the group consisting of Vitamins A, C, D, E, and B complex; and at least one mineral selected from the group consisting of calcium, magnesium, zinc, manganese, sodium, potassium, phosphorus, copper, chloride, iodine, selenium, and iron.

141. A dietary supplement comprising said microbial oil or fraction thereof of claim 129.

142. The dietary supplement of claim 141 further comprising at least one macronutrient selected from the group consisting of coconut oil, soy oil, canola oil, mono- and diglycerides, glucose, edible lactose, electro dialysed whey, electro dialysed skim milk, milk whey, soy protein, and other protein hydrolysates.

143. The dietary supplement of claim 142 further comprising at least one vitamin selected from the group consisting of Vitamins A, C, D, E, and B complex; and at least one mineral selected from the group consisting of calcium, magnesium, zinc, manganese, sodium, potassium, phosphorus, copper, chloride, iodine, selenium, and iron.

144. The dietary supplement of claim 143 wherein said dietary supplement is administered to a human or an animal.

145. A dietary substitute comprising said microbial oil or fraction thereof of claim 129.

146. The dietary substitute of claim 145 further comprising at least one macronutrient selected from the group consisting of coconut oil, soy oil, canola oil, mono- and diglycerides, glucose, edible lactose, electro dialysed whey, electro dialysed skim milk, milk whey, soy protein, and other protein hydrolysates.

147. The dietary substitute of claim 146 further comprising at least one vitamin selected from the group consisting of Vitamins A, C, D, E, and B complex; and at least one mineral selected from the group consisting of calcium, magnesium, zinc, manganese, sodium, potassium, phosphorus, copper, chloride, iodine, selenium, and iron.

148. The dietary substitute of claim 145 wherein said dietary substitute is administered to a human or animal.

149. A method of treating a patient having a condition caused by insufficient intake or production of polyunsaturated fatty acids comprising administering to said patients said dietary substitute of claim 148 in an amount sufficient to effect said treatment.

150. The method of claim 149 wherein said dietary substitute is administered enterally or parenterally.

151. A cosmetic comprising said microbial oil or fraction thereof of claim 129.

152. The cosmetic of claim 151 wherein said cosmetic is applied topically.

153. The pharmaceutical composition of claim 131 wherein said pharmaceutical composition is administered to a human or an animal.

154. An animal feed comprising said microbial oil or fraction thereof of claim 129.

155. A method for producing an oil or fraction thereof comprising growing one or more transgenic microbial cells under suitable conditions whereby said cells express one or more transgenic polypeptides wherein the sequence of said one or more polypeptides comprises a sequence selected from the group consisting of SEQ ID NO:4, SEQ ID NO:20, SEQ ID NO:22, SEQ ID NO:24 and SEQ ID NO:26.

156. A microbial oil or fraction thereof produced according to the method of claim 155.

157. A method of treating or preventing malnutrition comprising administering said microbial oil of claim 156 to a patient in need of said treatment or prevention in an amount sufficient to effect said treatment or prevention.

158. A pharmaceutical composition comprising said microbial oil or fraction of claim 156 and a pharmaceutically acceptable carrier.

159. The pharmaceutical composition of claim 158 wherein said pharmaceutical composition is in the form of a solid or a liquid.

160. The pharmaceutical composition of claim 158 wherein said pharmaceutical composition is in a capsule or tablet form.

161. The pharmaceutical composition of claim 158 further comprising at least one nutrient selected from the group consisting of a vitamin, a mineral,

a carbohydrate, a sugar, an amino acid, a free fatty acid, a phospholipid, an antioxidant, and a phenolic compound.

162. A nutritional formula comprising said microbial oil or fraction thereof of claim 156.

163. The nutritional formula of claim 162 wherein said nutritional formula is selected from the group consisting of an infant formula, a dietary supplement, and a dietary substitute.

164. The nutritional formula of claim 162 wherein said infant formula, dietary supplement or dietary supplement is in the form of a liquid or a solid.

165. An infant formula comprising said microbial oil or fraction thereof of claim 156.

166. The infant formula of claim 165 further comprising at least one macronutrient selected from the group consisting of coconut oil, soy oil, canola oil, mono- and diglycerides, glucose, edible lactose, electrodialysed whey, electrodialysed skim milk, milk whey, soy protein, and other protein hydrolysates.

167. The infant formula of claim 166 further comprising at least one vitamin selected from the group consisting of Vitamins A, C, D, E, and B complex; and at least one mineral selected from the group consisting of calcium, magnesium, zinc, manganese, sodium, potassium, phosphorus, copper, chloride, iodine, selenium, and iron.

168. A dietary supplement comprising said microbial oil or fraction thereof of claim 156.

169. The dietary supplement of claim 168 further comprising at least one macronutrient selected from the group consisting of coconut oil, soy oil, canola oil, mono- and diglycerides, glucose, edible lactose, electro dialysed whey, electro dialysed skim milk, milk whey, soy protein, and other protein hydrolysates.

170. The dietary supplement of claim 169 further comprising at least one vitamin selected from the group consisting of Vitamins A, C, D, E, and B complex; and at least one mineral selected from the group consisting of calcium, magnesium, zinc, manganese, sodium, potassium, phosphorus, copper, chloride, iodine, selenium, and iron.

171. The dietary supplement of claim 170 wherein said dietary supplement is administered to a human or an animal.

172. A dietary substitute comprising said microbial oil or fraction thereof of claim 156.

173. The dietary substitute of claim 172 further comprising at least one macronutrient selected from the group consisting of coconut oil, soy oil, canola oil, mono- and diglycerides, glucose, edible lactose, electro dialysed whey, electro dialysed skim milk, milk whey, soy protein, and other protein hydrolysates.

174. The dietary substitute of claim 173 further comprising at least one vitamin selected from the group consisting of Vitamins A, C, D, E, and B complex; and at least one mineral selected from the group consisting of calcium, magnesium, zinc, manganese, sodium, potassium, phosphorus, copper, chloride, iodine, selenium, and iron.

175. The dietary substitute of claim 173 wherein said dietary substitute is administered to a human or animal.

176. A method of treating a patient having a condition caused by insufficient intake or production of polyunsaturated fatty acids comprising administering to said patient said dietary substitute of claim 172 in an amount sufficient to effect said treatment.

177. The method of claim 176 wherein said dietary substitute is administered enterally or parenterally.

178. A cosmetic comprising said microbial oil or fraction thereof of claim 156.

179. The cosmetic of claim 178 wherein said cosmetic is applied topically.

180. The pharmaceutical composition of claim 158 wherein said pharmaceutical composition is administered to a human or an animal.

181. An animal feed comprising said microbial oil or fraction thereof of claim 156.

182. An isolated nucleotide sequence comprising a nucleotide sequence selected from the group consisting of SEQ ID NO:19, SEQ ID NO:21, SEQ ID NO:23 and SEQ ID NO:25.

183. An isolated and purified polypeptide wherein said polypeptide comprises a sequence selected from the group consisting of SEQ ID NO:20, SEQ ID NO:22, SEQ ID NO:24 and SEQ ID NO:26.

184. A method for producing an fatty acid comprising the steps of: growing microbial cells which contain one or more transgenes which encode a transgene expression product under conditions whereby said one or more transgenes are expressed, whereby long chain polyunsaturated fatty acid biosynthesis in said cells is altered whereby said transgene comprises a nucleotide sequence which encodes a polypeptide wherein the sequence of the polypeptide comprises a sequence selected from the group consisting of SEQ ID NO:4, SEQ ID NO:20, SEQ ID NO:22, SEQ ID NO:24 and SEQ ID NO:26.

185. A fatty acid produced according to the method of claim 184.

186. A fatty acid produced according to the method of claim 65.

187. A method for producing fatty acid comprising growing one or more transgenic microbial cells under suitable conditions whereby said cells express a transgenic polypeptide wherein the sequence of said polypeptide comprises a sequence selected from the group consisting of residues 50-53, 39-43, 172-176, 204-213 and 390-402 of SEQ ID NO:2

188. A fatty acid produced according to claim 187. --

REMARKS

In advance of prosecution, Applicants request entry of the present preliminary amendment. Applicants have canceled claims 1-64, amended claims 65-66, 69, 82, 86-88, 93-96, and 98, and added new claims 99 to 187. The claims have been amended in order to remove the multiple dependent claims in the application as filed and to add additional claims to more clearly define the invention. No new matter has been added.

Early and favorable action is requested.

Respectfully submitted,
LIMBACH & LIMBACH L.L.P.

Dated: August 5, 1999

By: Michael R. Ward

Michael R. Ward

Reg. No. 38,651

Tel. No. 415/433-4150

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PATENT COOPERATION TREATY

EUROPEAN PATENT OFFICE
INTERNATIONAL SEARCHING AUTHORITY

Docket No.: CGAB-210 PCT

International Application No.: PCT/US98/07126

International Filing Date: 10 April 1998 (10.04.98)

Title: **METHODS AND COMPOSITIONS FOR SYNTHESIS OF
LONG CHAIN POLYUNSATURATED FATTY ACIDS**

Applicants: CALGENE LLC and ABBOTT LABORATORIES et al.

**RESPONSE TO INVITATION TO FURNISH
NUCLEOTIDE AND/OR AMINO ACID SEQUENCE LISTING**

European Patent Office
International Searching Authority
P.B. 5818
Patentlaan 2
NL-2280 HV Rijswijk
NETHERLANDS

Attention: Zorka Bota, Authorized Officer

Sir:

In response to the Invitation to Furnish Nucleotide
And/Or Amino Acid Sequence Listing mailed May 27, 1998,
Applicants hereby submit the following documents for
filing in connection with the above-identified
International Application:

- (1) Revised paper copy of Sequence Listing.
- (2) Revised copy of Sequence Listing in computer
readable format.

Applicants assert that the revised Sequence Listing
submitted herewith complies with WIPO Standard ST. 23 in a
machine readable form provided, under Section 208, in
Annex C of the *Administrative Instructions*. The Sequence
Listing has been modified to replace the sequence codons
"Xxx" and "****" with "Xaa." This change in the Sequence

Listing is a correction within the meaning of Rule 26.4 PCT and is not a rectification within the meaning of Rule 91.1 PCT.

Applicants assert that the paper copy and the computer readable format copy submitted herewith are identical. In addition, since the revised Sequence Listing is merely a correction in format of the previously submitted sequence, the revised Sequence Listing does not go beyond the disclosure in the International Application as filed.

Respectfully submitted,

LIMBACH & LIMBACH L.L.P.

Date: July 13, 1998

By: Michael R. Ward
Michael R. Ward
2001 Ferry Building
San Francisco, CA 94111-4262
(415) 433-4150
Attorneys for Applicants

CGAB-210 PCT

METHODS AND COMPOSITIONS FOR SYNTHESIS OF LONG CHAIN POLYUNSATURATED FATTY ACIDS

RELATED APPLICATIONS

5 This application is a continuation-in-part application of United States
Patent Application Serial No. 08/834,655 filed April 11, 1997.

INTRODUCTION

Field of the Invention

10 This invention relates to modulating levels of enzymes and/or enzyme
components relating to production of long chain poly-unsaturated fatty acids
(PUFAs) in a microorganism or animal.

Background

15 Two main families of polyunsaturated fatty acids (PUFAs) are the $\omega 3$
fatty acids, exemplified by eicosapentaenoic acid (EPA), and the $\omega 6$ fatty acids,
exemplified by arachidonic acid (ARA). PUFAs are important components of
the plasma membrane of the cell, where they may be found in such forms as
phospholipids. PUFAs are necessary for proper development, particularly in the
developing infant brain, and for tissue formation and repair. PUFAs also serve
as precursors to other molecules of importance in human beings and animals,
20 including the prostacyclins, eicosanoids, leukotrienes and prostaglandins. Four
major long chain PUFAs of importance include docosahexaenoic acid (DHA)
and EPA, which are primarily found in different types of fish oil, γ -linolenic
acid (GLA), which is found in the seeds of a number of plants, including
evening primrose (*Oenothera biennis*), borage (*Borago officinalis*) and black
25 currants (*Ribes nigrum*), and stearidonic acid (SDA), which is found in marine
oils and plant seeds. Both GLA and another important long chain PUFA,
arachidonic acid (ARA), are found in filamentous fungi. ARA can be purified
from animal tissues including liver and adrenal gland. GLA, ARA, EPA and

SDA are themselves, or are dietary precursors to, important long chain fatty acids involved in prostaglandin synthesis, in treatment of heart disease, and in development of brain tissue.

For DHA, a number of sources exist for commercial production including a variety of marine organisms, oils obtained from cold water marine fish, and egg yolk fractions. For ARA, microorganisms including the genera *Mortierella*, *Entomophthora*, *Phytium* and *Porphyridium* can be used for commercial production. Commercial sources of SDA include the genera *Trichodesma* and *Echium*. Commercial sources of GLA include evening primrose, black currants and borage. However, there are several disadvantages associated with commercial production of PUFAs from natural sources. Natural sources of PUFAs, such as animals and plants, tend to have highly heterogeneous oil compositions. The oils obtained from these sources therefore can require extensive purification to separate out one or more desired PUFAs or to produce an oil which is enriched in one or more PUFA. Natural sources also are subject to uncontrollable fluctuations in availability. Fish stocks may undergo natural variation or may be depleted by overfishing. Fish oils have unpleasant tastes and odors, which may be impossible to economically separate from the desired product, and can render such products unacceptable as food supplements. Animal oils, and particularly fish oils, can accumulate environmental pollutants. Weather and disease can cause fluctuation in yields from both fish and plant sources. Cropland available for production of alternate oil-producing crops is subject to competition from the steady expansion of human populations and the associated increased need for food production on the remaining arable land. Crops which do produce PUFAs, such as borage, have not been adapted to commercial growth and may not perform well in monoculture. Growth of such crops is thus not economically competitive where more profitable and better established crops can be grown. Large scale fermentation of organisms such as *Mortierella* is also expensive. Natural animal tissues contain low amounts of ARA and are difficult to process. Microorganisms such as *Porphyridium* and *Mortierella* are difficult to cultivate on a commercial scale.

Dietary supplements and pharmaceutical formulations containing PUFAs can retain the disadvantages of the PUFA source. Supplements such as fish oil capsules can contain low levels of the particular desired component and thus require large dosages. High dosages result in ingestion of high levels of undesired components, including contaminants. Unpleasant tastes and odors of the supplements can make such regimens undesirable, and may inhibit compliance by the patient. Care must be taken in providing fatty acid supplements, as overaddition may result in suppression of endogenous biosynthetic pathways and lead to competition with other necessary fatty acids in various lipid fractions *in vivo*, leading to undesirable results. For example, Eskimos having a diet high in ω 3 fatty acids have an increased tendency to bleed (U.S. Pat. No. 4,874,603).

A number of enzymes are involved in PUFA biosynthesis. Linoleic acid (LA, 18:2 Δ 9, 12) is produced from oleic acid (18:1 Δ 9) by a Δ 12-desaturase. GLA (18:3 Δ 6, 9, 12) is produced from linoleic acid (LA, 18:2 Δ 9, 12) by a Δ 6-desaturase. ARA (20:4 Δ 5, 8, 11, 14) production from dihomo- γ -linolenic acid (DGLA, 20:3 Δ 8, 11, 14) is catalyzed by a Δ 5-desaturase. However, animals cannot desaturate beyond the Δ 9 position and therefore cannot convert oleic acid (18:1 Δ 9) into linoleic acid (18:2 Δ 9, 12). Likewise, α -linolenic acid (ALA, 18:3 Δ 9, 12, 15) cannot be synthesized by mammals. Other eukaryotes, including fungi and plants, have enzymes which desaturate at positions Δ 12 and Δ 15. The major poly-unsaturated fatty acids of animals therefore are either derived from diet and/or from desaturation and elongation of linoleic acid (18:2 Δ 9, 12) or α -linolenic acid (18:3 Δ 9, 12, 15). Therefore it is of interest to obtain genetic material involved in PUFA biosynthesis from species that naturally produce these fatty acids and to express the isolated material in a microbial or animal system which can be manipulated to provide production of commercial quantities of one or more PUFAs. Thus there is a need for fatty acid desaturases, genes encoding them, and recombinant methods of producing them. A need further exists for oils containing higher relative proportions of and/or

enriched in specific PUFAs. A need also exists for reliable economical methods of producing specific PUFAs.

Relevant Literature

Production of γ -linolenic acid by a $\Delta 6$ -desaturase is described in USPN 5,552,306. Production of 8, 11-eicosadienoic acid using *Mortierella alpina* is disclosed in USPN 5,376,541. Production of docosahexaenoic acid by dinoflagellates is described in USPN 5,407,957. Cloning of a $\Delta 6$ -palmitoyl-acyl carrier protein desaturase is described in PCT publication WO 96/13591 and USPN 5,614,400. Cloning of a $\Delta 6$ -desaturase from borage is described in PCT publication WO 96/21022. Cloning of $\Delta 9$ -desaturases is described in the published patent applications PCT WO 91/13972, EP 0 550 162 A1, EP 0 561 569 A2, EP 0 644 263 A2, and EP 0 736 598 A1, and in USPN 5,057,419. Cloning of $\Delta 12$ -desaturases from various organisms is described in PCT publication WO 94/11516 and USPN 5,443,974. Cloning of $\Delta 15$ -desaturases from various organisms is described in PCT publication WO 93/11245. All publications and U.S. patents or applications referred to herein are hereby incorporated in their entirety by reference.

SUMMARY OF THE INVENTION

Novel compositions and methods are provided for preparation of poly-unsaturated long chain fatty acids. The compositions include nucleic acid encoding a $\Delta 6$ - and $\Delta 12$ - desaturase and/or polypeptides having $\Delta 6$ - and/or $\Delta 12$ -desaturase activity, the polypeptides, and probes isolating and detecting the same. The methods involve growing a host microorganism or animal expressing an introduced gene or genes encoding at least one desaturase, particularly a $\Delta 6$ -, $\Delta 9$ -, $\Delta 12$ - or $\Delta 15$ -desaturase. The methods also involve the use of antisense constructs or gene disruptions to decrease or eliminate the expression level of undesired desaturases. Regulation of expression of the desaturase polypeptide(s) provides for a relative increase in desired desaturated PUFAs as a result of altered concentrations of enzymes and substrates involved

in PUFA biosynthesis. The invention finds use, for example, in the large scale production of GLA, DGLA, ARA, EPA, DHA and SDA.

In a preferred embodiment of the invention, an isolated nucleic acid comprising: a nucleotide sequence depicted in Figure 3A-E (SEQ ID NO: 1) or Figure 5A-D (SEQ ID NO: 3), a polypeptide encoded by a nucleotide sequence according Figure 3A-E (SEQ ID NO: 1) or Figure 5A-D (SEQ ID NO: 3), and a purified or isolated polypeptide comprising an amino acid sequence depicted in Figure 3A-E (SEQ ID NO: 2) or Figure 5A-D (SEQ ID NO: 4). In another embodiment of the invention, provided is an isolated nucleic acid encoding a polypeptide having an amino acid sequence depicted in Figure 3A-E (SEQ ID NO: 2) or Figure 5A-D (SEQ ID NO: 4).

Also provided is an isolated nucleic acid comprising a nucleotide sequence which encodes a polypeptide which desaturates a fatty acid molecule at carbon 6 or 12 from the carboxyl end, wherein said nucleotide sequence has an average A/T content of less than about 60%. In a preferred embodiment, the isolated nucleic acid is derived from a fungus, such as a fungus of the genus *Mortierella*. More preferred is a fungus of the species *Mortierella alpina*.

In another preferred embodiment of the invention, an isolated nucleic acid is provided wherein the nucleotide sequence of the nucleic acid is depicted in Figure 3A-E (SEQ ID NO: 1) or Figure 5A-D (SEQ ID NO: 3). The invention also provides an isolated or purified polypeptide which desaturates a fatty acid molecule at carbon 6 or 12 from the carboxyl end, wherein the polypeptide is a eukaryotic polypeptide or is derived from a eukaryotic polypeptide, where a preferred eukaryotic polypeptide is derived from a fungus.

The present invention further includes a nucleic acid sequence which hybridizes to Figure 3A-E (SEQ ID NO: 1) or Figure 5A-D (SEQ ID NO: 3). Preferred is an isolated nucleic acid having a nucleotide sequence with at least about 50% homology to Figure 3A-E (SEQ ID NO: 1) or Figure 5A-D (SEQ ID NO: 3). The invention also includes an isolated nucleic acid having a nucleotide sequence with at least about 50% homology to Figure 3A-E (SEQ ID NO: 1) or Figure 5A-D (SEQ ID NO: 3). In a preferred embodiment, the

nucleic acid of the invention includes a nucleotide sequence which encodes an amino acid sequence depicted in Figure 3A-D (SEQ ID NO: 2) which is selected from the group consisting of amino acid residues 50-53, 39-43, 172-176, 204-213, and 390-402.

Also provided by the present invention is a nucleic acid construct comprising a nucleotide sequence depicted in a Figure 3A-E (SEQ ID NO: 1) or Figure 5A-D (SEQ ID NO: 3) linked to a heterologous nucleic acid. In another embodiment, a nucleic acid construct is provided which comprises a nucleotide sequence depicted in a Figure 3A-E (SEQ ID NO: 1) or Figure 5A-D (SEQ ID NO: 3) operably associated with an expression control sequence functional in a host cell. The host cell is either eukaryotic or prokaryotic. Preferred eukaryotic host cells are those selected from the group consisting of a mammalian cell, an insect cell, a fungal cell, and an algae cell. Preferred mammalian cells include an avian cell, a preferred fungal cell includes a yeast cell, and a preferred algae cell is a marine algae cell. Preferred prokaryotic cells include those selected from the group consisting of a bacteria, a cyanobacteria, cells which contain a bacteriophage, and/or a virus. The DNA sequence of the recombinant host cell preferably contains a promoter which is functional in the host cell, which promoter is preferably inducible. In a more preferred embodiment, the microbial cell is a fungal cell of the genus *Mortierella*, with a more preferred fungus is of the species *Mortierella alpina*.

In addition, the present invention provides a nucleic acid construct comprising a nucleotide sequence which encodes a polypeptide comprising an amino acid sequence which corresponds to or is complementary to an amino acid sequence depicted in Figure 3A-E (SEQ ID NO: 2) or Figure 5A-D (SEQ ID NO: 4), wherein the nucleic acid is operably associated with an expression control sequence functional in a microbial cell, wherein the nucleotide sequence encodes a functionally active polypeptide which desaturates a fatty acid molecule at carbon 6 or carbon 12 from the carboxyl end of a fatty acid molecule. Another embodiment of the present invention is a nucleic acid construct comprising a nucleotide sequence which encodes a functionally active $\Delta 6$ -desaturase having an amino acid sequence which corresponds to or is

complementary to all of or a portion of an amino acid sequence depicted in a Figure 3A-E (SEQ ID NO: 2), wherein the nucleotide sequence is operably associated with a transcription control sequence functional in a host cell.

Yet another embodiment of the present invention is a nucleic acid construct comprising a nucleotide sequence which encodes a functionally active $\Delta 12$ -desaturase having an amino acid sequence which corresponds to or is complementary to all of or a portion of an amino acid sequence depicted in a Figure 5A-D (SEQ ID NO: 4), wherein the nucleotide sequence is operably associated with a transcription control sequence functional in a host cell. The host cell, is either a eukaryotic or prokaryotic host cell. Preferred eukaryotic host cells are those selected from the group consisting of a mammalian cell, an insect cell, a fungal cell, and an algae cell. Preferred mammalian cells include an avian cell, a preferred fungal cell includes a yeast cell, and a preferred algae cell is a marine algae cell. Preferred prokaryotic cells include those selected from the group consisting of a bacteria, a cyanobacteria, cells which contain a bacteriophage, and/or a virus. The DNA sequence of the recombinant host cell preferably contains a promoter which is functional in the host cell and which preferably is inducible. A preferred recombinant host cell is a microbial cell such as a yeast cell, such as a *Saccharomyces* cell.

The present invention also provides a recombinant microbial cell comprising at least one copy of a nucleic acid which encodes a functionally active *Mortierella alpina* fatty acid desaturase having an amino acid sequence as depicted in Figure 3A-E (SEQ ID NO: 2), wherein the cell or a parent of the cell was transformed with a vector comprising said DNA sequence, and wherein the DNA sequence is operably associated with an expression control sequence. In a preferred embodiment, the cell is a microbial cell which is enriched in 18:2 fatty acids, particularly where the microbial cell is from a genus selected from the group consisting of a prokaryotic cell and eukaryotic cell. In another preferred embodiment, the microbial cell according to the invention includes an expression control sequence which is endogenous to the microbial cell.

Also provided by the present invention is a method for production of GLA in a host cell, where the method comprises growing a host culture having a plurality of host cells which contain one or more nucleic acids encoding a polypeptide which converts LA to GLA, wherein said one or more nucleic acids is operably associated with an expression control sequence, under conditions whereby said one or more nucleic acids are expressed, whereby GLA is produced in the host cell. In several preferred embodiments of the methods, the polypeptide employed in the method is a functionally active enzyme which desaturates a fatty acid molecule at carbon 6 from the carboxyl end of a fatty acid molecule; the said one or more nucleic acids is derived from a *Mortierella alpina*; the substrate for the polypeptide is exogenously supplied; the host cells are microbial cells; the microbial cells are yeast cells, such as *Saccharomyces* cells; and the growing conditions are inducible.

Also provided is an oil comprising one or more PUFA, wherein the amount of said one or more PUFAs is approximately 0.3-30% arachidonic acid (ARA), approximately 0.2-30% dihomo- γ -linolenic acid (DGLA), and approximately 0.2-30% γ -linoleic acid (GLA). A preferred oil of the invention is one in which the ratio of ARA:DGLA:GLA is approximately 1.0:19.0:30 to 6.0:1.0:0.2. Another preferred embodiment of the invention is a pharmaceutical composition comprising the oils in a pharmaceutically acceptable carrier. Further provided is a nutritional composition comprising the oils of the invention. The nutritional compositions of the invention preferably are administered to a mammalian host parenterally or internally. A preferred composition of the invention for internal consumption is an infant formula. In a preferred embodiment, the nutritional compositions of the invention are in a liquid form or a solid form, and can be formulated in or as a dietary supplement, and the oils provided in encapsulated form. The oils of the invention can be free of particular components of other oils and can be derived from a microbial cell, such as a yeast cell.

The present invention further provides a method for desaturating a fatty acid. In a preferred embodiment the method comprises culturing a recombinant microbial cell according to the invention under conditions suitable for

expression of a polypeptide encoded by said nucleic acid, wherein the host cell further comprises a fatty acid substrate of said polypeptide. Also provided is a fatty acid desaturated by such a method, and an oil composition comprising a fatty acid produced according to the methods of the invention.

5 The present invention further includes a purified nucleotide sequence or polypeptide sequence that is substantially related or homologous to the nucleotide and peptide sequences presented in SEQ ID NO:1 - SEQ ID NO:40. The present invention is further directed to methods of using the sequences presented in SEQ ID NO:1 to SEQ ID NO:40 as probes to identify related
10 sequences, as components of expression systems and as components of systems useful for producing transgenic oil.

 The present invention is further directed to formulas, dietary supplements or dietary supplements in the form of a liquid or a solid containing the long chain fatty acids of the invention. These formulas and supplements
15 may be administered to a human or an animal.

 The formulas and supplements of the invention may further comprise at least one macronutrient selected from the group consisting of coconut oil, soy oil, canola oil, mono- and diglycerides, glucose, edible lactose, electro dialysed whey, electro dialysed skim milk, milk whey, soy protein, and other protein
20 hydrolysates.

 The formulas of the present invention may further include at least one vitamin selected from the group consisting of Vitamins A, C, D, E, and B complex; and at least one mineral selected from the group consisting of calcium, magnesium, zinc, manganese, sodium, potassium, phosphorus, copper,
25 chloride, iodine, selenium, and iron.

 The present invention is further directed to a method of treating a patient having a condition caused by insufficient intake or production of polyunsaturated fatty acids comprising administering to the patient a dietary substitute of the invention in an amount sufficient to effect treatment of the patient.

30 The present invention is further directed to cosmetic and pharmaceutical compositions of the material of the invention.

The present invention is further directed to transgenic oils in pharmaceutically acceptable carriers. The present invention is further directed to nutritional supplements, cosmetic agents and infant formulae containing transgenic oils.

5 The present invention is further directed to a method for obtaining altered long chain polyunsaturated fatty acid biosynthesis comprising the steps of: growing a microbe having cells which contain a transgene which encodes a transgene expression product which desaturates a fatty acid molecule at carbon 6 or 12 from the carboxyl end of said fatty acid molecule, wherein the transgene is operably associated with an expression control sequence, under conditions
10 whereby the transgene is expressed, whereby long chain polyunsaturated fatty acid biosynthesis in the cells is altered.

 The present invention is further directed toward pharmaceutical compositions comprising at least one nutrient selected from the group consisting
15 of a vitamin, a mineral, a carbohydrate, a sugar, an amino acid, a free fatty acid, a phospholipid, an antioxidant, and a phenolic compound.

BRIEF DESCRIPTION OF THE DRAWINGS

 Figure 1 shows possible pathways for the synthesis of arachidonic acid
20 (20:4 Δ 5, 8, 11, 14) and stearidonic acid (18:4 Δ 6, 9, 12, 15) from palmitic acid (C_{16}) from a variety of organisms, including algae, *Mortierella* and humans. These PUFAs can serve as precursors to other molecules important for humans and other animals, including prostacyclins, leukotrienes, and prostaglandins, some of which are shown.

25 Figure 2 shows possible pathways for production of PUFAs in addition to ARA, including EPA and DHA, again compiled from a variety of organisms.

 Figure 3A-E shows the DNA sequence of the *Mortierella alpina* Δ 6-desaturase and the deduced amino acid sequence:

 Figure 3A-E (SEQ ID NO 1 Δ 6 DESATURASE cDNA)

Figure 3A-E (SEQ ID NO 2 $\Delta 6$ DESATURASE AMINO ACID)

Figure 4 shows an alignment of a portion of the *Mortierella alpina* $\Delta 6$ -desaturase amino acid sequence with other related sequences.

5 Figure 5A-D shows the DNA sequence of the *Mortierella alpina* $\Delta 12$ -desaturase and the deduced amino acid sequence:

Figure 5A-D (SEQ ID NO 3 $\Delta 12$ DESATURASE cDNA)

Figure 5A-D (SEQ ID NO 4 $\Delta 12$ DESATURASE AMINO ACID).

Figures 6A and 6B show the effect of different expression constructs on expression of GLA in yeast.

10 Figures 7A and 7B show the effect of host strain on GLA production.

Figures 8A and 8B show the effect of temperature on GLA production in *S. cerevisiae* strain SC334.

Figure 9 shows alignments of the protein sequence of the Ma 29 and contig 253538a.

15 Figure 10 shows alignments of the protein sequence of Ma 524 and contig 253538a.

BRIEF DESCRIPTION OF THE SEQUENCE LISTINGS

SEQ ID NO:1 shows the DNA sequence of the *Mortierella alpina* $\Delta 6$ -desaturase.

20 SEQ ID NO:2 shows the protein sequence of the *Mortierella alpina* $\Delta 6$ -desaturase.

SEQ ID NO:3 shows the DNA sequence of the *Mortierella alpina* $\Delta 12$ -desaturase.

25 SEQ ID NO:4 shows the protein sequence of the *Mortierella alpina* $\Delta 12$ -desaturase.

SEQ ID NO:5-11 show various desaturase sequences.

SEQ ID NO:13-18 show various PCR primer sequences.

SEQ ID NO:19 and SEQ ID NO:20 show the nucleotide and amino acid sequence of a *Dictyostelium discoideum* desaturase.

SEQ ID NO:21 and SEQ ID NO:22 show the nucleotide and amino acid sequence of a *Phaeodactylum tricornutum* desaturase.

SEQ ID NO:23-26 show the nucleotide and deduced amino acid sequence of a *Schizochytrium* cDNA clone.

SEQ ID NO: 27-33 show nucleotide sequences for human desaturases.

SEQ ID NO:34 - SEQ ID NO:40 show peptide sequences for human desaturases.

DESCRIPTION OF THE PREFERRED EMBODIMENTS

In order to ensure a complete understanding of the invention, the following definitions are provided:

Δ 5-Desaturase: Δ 5 desaturase is an enzyme which introduces a double bond between carbons 5 and 6 from the carboxyl end of a fatty acid molecule.

Δ 6-Desaturase: Δ 6-desaturase is an enzyme which introduces a double bond between carbons 6 and 7 from the carboxyl end of a fatty acid molecule.

Δ 9-Desaturase: Δ 9-desaturase is an enzyme which introduces a double bond between carbons 9 and 10 from the carboxyl end of a fatty acid molecule.

Δ 12-Desaturase: Δ 12-desaturase is an enzyme which introduces a double bond between carbons 12 and 13 from the carboxyl end of a fatty acid molecule.

Fatty Acids: Fatty acids are a class of compounds containing a long hydrocarbon chain and a terminal carboxylate group. Fatty acids include the following:

Fatty Acid		
12:0	lauric acid	
16:0	palmitic acid	

Fatty Acid		
16:1	palmitoleic acid	
18:0	stearic acid	
18:1	oleic acid	$\Delta 9$ -18:1
18:2 $\Delta 5,9$	taxoleic acid	$\Delta 5,9$ -18:2
18:2 $\Delta 6,9$	6,9-octadecadienoic acid	$\Delta 6,9$ -18:2
18:2	Linolenic acid	$\Delta 9,12$ -18:2 (LA)
18:3 $\Delta 6,9,12$	Gamma-linolenic acid	$\Delta 6,9,12$ -18:3 (GLA)
18:3 $\Delta 5,9,12$	Pinolenic acid	$\Delta 5,9,12$ -18:3
18:3	alpha-linoleic acid	$\Delta 9,12,15$ -18:3 (ALA)
18:4	stearidonic acid	$\Delta 6,9,12,15$ -18:4 (SDA)
20:0	Arachidic acid	
20:1	Eicosenic Acid	
22:0	behehic acid	
22:1	erucic acid	
22:2	docasadienoic acid	
20:4 $\omega 6$	arachidonic acid	$\Delta 5,8,11,14$ -20:4 (ARA)
20:3 $\omega 6$	$\omega 6$ -eicosatrienoic dihomo-gamma linolenic	$\Delta 8,11,14$ -20:3 (DGLA)
20:5 $\omega 3$	Eicosapentanoic (Timnodonic acid)	$\Delta 5,8,11,14,17$ -20:5 (EPA)
20:3 $\omega 3$	$\omega 3$ -eicosatrienoic	$\Delta 11,16,17$ -20:3
20:4 $\omega 3$	$\omega 3$ -eicosatetraenoic	$\Delta 8,11,14,17$ -20:4
22:5 $\omega 3$	Docosapentaenoic	$\Delta 7,10,13,16,19$ -22:5 ($\omega 3$ DPA)
22:6 $\omega 3$	Docosahexaenoic (cervonic acid)	$\Delta 4,7,10,13,16,19$ -22:6 (DHA)
24:0	Lignoceric acid	

5 Taking into account these definitions, the present invention is directed to novel DNA sequences, DNA constructs, methods and compositions are provided which permit modification of the poly-unsaturated long chain fatty acid content of, for example, microbial cells or animals. Host cells are manipulated to express a sense or antisense transcript of a DNA encoding a polypeptide(s) which catalyzes the desaturation of a fatty acid. The substrate(s) for the expressed enzyme may be produced by the host cell or may be exogenously supplied. To achieve expression, the transformed DNA is

operably associated with transcriptional and translational initiation and termination regulatory regions that are functional in the host cell. Constructs comprising the gene to be expressed can provide for integration into the genome of the host cell or can autonomously replicate in the host cell. For production of linoleic acid (LA), the expression cassettes generally used include a cassette which provides for $\Delta 12$ -desaturase activity, particularly in a host cell which produces or can take up oleic acid (U.S. Patent No. 5,443,974). Production of LA also can be increased by providing an expression cassette for a $\Delta 9$ -desaturase where that enzymatic activity is limiting. For production of ALA, the expression cassettes generally used include a cassette which provides for $\Delta 15$ - or $\omega 3$ -desaturase activity, particularly in a host cell which produces or can take up LA. For production of GLA or SDA, the expression cassettes generally used include a cassette which provides for $\Delta 6$ -desaturase activity, particularly in a host cell which produces or can take up LA or ALA, respectively. Production of $\omega 6$ -type unsaturated fatty acids, such as LA or GLA, is favored in a host microorganism or animal which is incapable of producing ALA. The host ALA production can be removed, reduced and/or inhibited by inhibiting the activity of a $\Delta 15$ - or $\omega 3$ - type desaturase (see Figure 2). This can be accomplished by standard selection, providing an expression cassette for an antisense $\Delta 15$ or $\omega 3$ transcript, by disrupting a target $\Delta 15$ - or $\omega 3$ -desaturase gene through insertion, deletion, substitution of part or all of the target gene, or by adding an inhibitor of $\Delta 15$ - or $\omega 3$ -desaturase. Similarly, production of LA or ALA is favored in a microorganism or animal having $\Delta 6$ -desaturase activity by providing an expression cassette for an antisense $\Delta 6$ transcript, by disrupting a $\Delta 6$ -desaturase gene, or by use of a $\Delta 6$ -desaturase inhibitor.

MICROBIAL PRODUCTION OF FATTY ACIDS

Microbial production of fatty acids has several advantages over purification from natural sources such as fish or plants. Many microbes are known with greatly simplified oil compositions compared with those of higher organisms, making purification of desired components easier. Microbial production is not subject to fluctuations caused by external variables such as

weather and food supply. Microbially produced oil is substantially free of contamination by environmental pollutants. Additionally, microbes can provide PUFAs in particular forms which may have specific uses. For example, *Spirulina* can provide PUFAs predominantly at the first and third positions of triglycerides; digestion by pancreatic lipases preferentially releases fatty acids from these positions. Following human or animal ingestion of triglycerides derived from *Spirulina*, these PUFAs are released by pancreatic lipases as free fatty acids and thus are directly available, for example, for infant brain development. Additionally, microbial oil production can be manipulated by controlling culture conditions, notably by providing particular substrates for microbially expressed enzymes, or by addition of compounds which suppress undesired biochemical pathways. In addition to these advantages, production of fatty acids from recombinant microbes provides the ability to alter the naturally occurring microbial fatty acid profile by providing new synthetic pathways in the host or by suppressing undesired pathways, thereby increasing levels of desired PUFAs, or conjugated forms thereof, and decreasing levels of undesired PUFAs.

PRODUCTION OF FATTY ACIDS IN ANIMALS

Production of fatty acids in animals also presents several advantages. Expression of desaturase genes in animals can produce greatly increased levels of desired PUFAs in animal tissues, making recovery from those tissues more economical. For example, where the desired PUFAs are expressed in the breast milk of animals, methods of isolating PUFAs from animal milk are well established. In addition to providing a source for purification of desired PUFAs, animal breast milk can be manipulated through expression of desaturase genes, either alone or in combination with other human genes, to provide animal milks substantially similar to human breast milk during the different stages of infant development. Humanized animal milks could serve as infant formulas where human nursing is impossible or undesired, or in cases of malnourishment or disease.

Depending upon the host cell, the availability of substrate, and the desired end product(s), several polypeptides, particularly desaturases, are of

interest. By "desaturase" is intended a polypeptide which can desaturate one or more fatty acids to produce a mono- or poly-unsaturated fatty acid or precursor thereof of interest. Of particular interest are polypeptides which can catalyze the conversion of stearic acid to oleic acid, of oleic acid to LA, of LA to ALA, of LA to GLA, or of ALA to SDA, which includes enzymes which desaturate at the $\Delta 9$, $\Delta 12$, ($\omega 6$), $\Delta 15$, ($\omega 3$) or $\Delta 6$ positions. By "polypeptide" is meant any chain of amino acids, regardless of length or post-translational modification, for example, glycosylation or phosphorylation. Considerations for choosing a specific polypeptide having desaturase activity include the pH optimum of the polypeptide, whether the polypeptide is a rate limiting enzyme or a component thereof, whether the desaturase used is essential for synthesis of a desired poly-unsaturated fatty acid, and/or co-factors required by the polypeptide. The expressed polypeptide preferably has parameters compatible with the biochemical environment of its location in the host cell. For example, the polypeptide may have to compete for substrate with other enzymes in the host cell. Analyses of the K_m and specific activity of the polypeptide in question therefore are considered in determining the suitability of a given polypeptide for modifying PUFA production in a given host cell. The polypeptide used in a particular situation is one which can function under the conditions present in the intended host cell but otherwise can be any polypeptide having desaturase activity which has the desired characteristic of being capable of modifying the relative production of a desired PUFA.

For production of linoleic acid from oleic acid, the DNA sequence used encodes a polypeptide having $\Delta 12$ -desaturase activity. For production of GLA from linoleic acid, the DNA sequence used encodes a polypeptide having $\Delta 6$ -desaturase activity. In particular instances, expression of $\Delta 6$ -desaturase activity can be coupled with expression of $\Delta 12$ -desaturase activity and the host cell can optionally be depleted of any $\Delta 15$ -desaturase activity present, for example by providing a transcription cassette for production of antisense sequences to the $\Delta 15$ -desaturase transcription product, by disrupting the $\Delta 15$ -desaturase gene, or by using a host cell which naturally has, or has been mutated to have, low $\Delta 15$ -desaturase activity. Inhibition of undesired desaturase pathways also can be

accomplished through the use of specific desaturase inhibitors such as those described in U.S. Patent No. 4,778,630. Also, a host cell for $\Delta 6$ -desaturase expression may have, or have been mutated to have, high $\Delta 12$ -desaturase activity. The choice of combination of cassettes used depends in part on the PUFA profile and/or desaturase profile of the host cell. Where the host cell expresses $\Delta 12$ -desaturase activity and lacks or is depleted in $\Delta 15$ -desaturase activity, overexpression of $\Delta 6$ -desaturase alone generally is sufficient to provide for enhanced GLA production. Where the host cell expresses $\Delta 9$ -desaturase activity, expression of a $\Delta 12$ - and a $\Delta 6$ -desaturase can provide for enhanced GLA production. When $\Delta 9$ -desaturase activity is absent or limiting, an expression cassette for $\Delta 9$ -desaturase can be used. A scheme for the synthesis of arachidonic acid ($20:4 \Delta^{5, 8, 11, 14}$) from stearic acid ($18:0$) is shown in Figure 2. A key enzyme in this pathway is a $\Delta 6$ -desaturase which converts the linoleic acid into γ -linolenic acid. Conversion of α -linolenic acid (ALA) to stearidonic acid by a $\Delta 6$ -desaturase also is shown.

SOURCES OF POLYPEPTIDES HAVING DESATURASE ACTIVITY

A source of polypeptides having desaturase activity and oligonucleotides encoding such polypeptides are organisms which produce a desired polyunsaturated fatty acid. As an example, microorganisms having an ability to produce GLA or ARA can be used as a source of $\Delta 6$ - or $\Delta 12$ - desaturase activity. Such microorganisms include, for example, those belonging to the genera *Mortierella*, *Conidiobolus*, *Pythium*, *Phytophthora*, *Penicillium*, *Porphyridium*, *Coidosporium*, *Mucor*, *Fusarium*, *Aspergillus*, *Rhodotorula*, and *Entomophthora*. Within the genus *Porphyridium*, of particular interest is *Porphyridium cruentum*. Within the genus *Mortierella*, of particular interest are *Mortierella elongata*, *Mortierella exigua*, *Mortierella hygrophila*, *Mortierella ramanniana*, var. *angulispora*, and *Mortierella alpina*. Within the genus *Mucor*, of particular interest are *Mucor circinelloides* and *Mucor javanicus*.

DNAs encoding desired desaturases can be identified in a variety of ways. As an example, a source of the desired desaturase, for example genomic

or cDNA libraries from *Mortierella*, is screened with detectable enzymatically- or chemically-synthesized probes, which can be made from DNA, RNA, or non-naturally occurring nucleotides, or mixtures thereof. Probes may be enzymatically synthesized from DNAs of known desaturases for normal or reduced-stringency hybridization methods. Oligonucleotide probes also can be used to screen sources and can be based on sequences of known desaturases, including sequences conserved among known desaturases, or on peptide sequences obtained from the desired purified protein. Oligonucleotide probes based on amino acid sequences can be degenerate to encompass the degeneracy of the genetic code, or can be biased in favor of the preferred codons of the source organism. Oligonucleotides also can be used as primers for PCR from reverse transcribed mRNA from a known or suspected source; the PCR product can be the full length cDNA or can be used to generate a probe to obtain the desired full length cDNA. Alternatively, a desired protein can be entirely sequenced and total synthesis of a DNA encoding that polypeptide performed.

Once the desired genomic or cDNA has been isolated, it can be sequenced by known methods. It is recognized in the art that such methods are subject to errors, such that multiple sequencing of the same region is routine and is still expected to lead to measurable rates of mistakes in the resulting deduced sequence, particularly in regions having repeated domains, extensive secondary structure, or unusual base compositions, such as regions with high GC base content. When discrepancies arise, resequencing can be done and can employ special methods. Special methods can include altering sequencing conditions by using: different temperatures; different enzymes; proteins which alter the ability of oligonucleotides to form higher order structures; altered nucleotides such as ITP or methylated dGTP; different gel compositions, for example adding formamide; different primers or primers located at different distances from the problem region; or different templates such as single stranded DNAs. Sequencing of mRNA also can be employed.

For the most part, some or all of the coding sequence for the polypeptide having desaturase activity is from a natural source. In some situations, however, it is desirable to modify all or a portion of the codons, for example, to

enhance expression, by employing host preferred codons. Host preferred codons can be determined from the codons of highest frequency in the proteins expressed in the largest amount in a particular host species of interest. Thus, the coding sequence for a polypeptide having desaturase activity can be synthesized in whole or in part. All or portions of the DNA also can be synthesized to remove any destabilizing sequences or regions of secondary structure which would be present in the transcribed mRNA. All or portions of the DNA also can be synthesized to alter the base composition to one more preferable in the desired host cell. Methods for synthesizing sequences and bringing sequences together are well established in the literature. *In vitro* mutagenesis and selection, site-directed mutagenesis, or other means can be employed to obtain mutations of naturally occurring desaturase genes to produce a polypeptide having desaturase activity *in vivo* with more desirable physical and kinetic parameters for function in the host cell, such as a longer half-life or a higher rate of production of a desired polyunsaturated fatty acid.

Mortierella alpina Desaturase

Of particular interest is the *Mortierella alpina* $\Delta 6$ -desaturase, which has 457 amino acids and a predicted molecular weight of 51.8 kD; the amino acid sequence is shown in Figure 3. The gene encoding the *Mortierella alpina* $\Delta 6$ -desaturase can be expressed in transgenic microorganisms or animals to effect greater synthesis of GLA from linoleic acid or of stearidonic acid from ALA. Other DNAs which are substantially identical to the *Mortierella alpina* $\Delta 6$ -desaturase DNA, or which encode polypeptides which are substantially identical to the *Mortierella alpina* $\Delta 6$ -desaturase polypeptide, also can be used. By substantially identical is intended an amino acid sequence or nucleic acid sequence exhibiting in order of increasing preference at least 60%, 80%, 90% or 95% homology to the *Mortierella alpina* $\Delta 6$ -desaturase amino acid sequence or nucleic acid sequence encoding the amino acid sequence. For polypeptides, the length of comparison sequences generally is at least 16 amino acids, preferably at least 20 amino acids, or most preferably 35 amino acids. For nucleic acids, the length of comparison sequences generally is at least 50 nucleotides,

preferably at least 60 nucleotides, and more preferably at least 75 nucleotides, and most preferably, 110 nucleotides. Homology typically is measured using sequence analysis software, for example, the Sequence Analysis software package of the Genetics Computer Group, University of Wisconsin Biotechnology Center, 1710 University Avenue, Madison, Wisconsin 53705, MEGAlign (DNASTar, Inc., 1228 S. Park St., Madison, Wisconsin 53715), and MacVector (Oxford Molecular Group, 2105 S. Bascom Avenue, Suite 200, Campbell, California 95008). Such software matches similar sequences by assigning degrees of homology to various substitutions, deletions, and other modifications. Conservative substitutions typically include substitutions within the following groups: glycine and alanine; valine, isoleucine and leucine; aspartic acid, glutamic acid, asparagine, and glutamine; serine and threonine; lysine and arginine; and phenylalanine and tyrosine. Substitutions may also be made on the basis of conserved hydrophobicity or hydrophilicity (Kyte and Doolittle, *J. Mol. Biol.* 157: 105-132, 1982), or on the basis of the ability to assume similar polypeptide secondary structure (Chou and Fasman, *Adv. Enzymol.* 47: 45-148, 1978).

Also of interest is the *Mortierella alpina* Δ 12-desaturase, the nucleotide and amino acid sequence of which is shown in Figure 5. The gene encoding the *Mortierella alpina* Δ 12-desaturase can be expressed in transgenic microorganisms or animals to effect greater synthesis of LA from oleic acid. Other DNAs which are substantially identical to the *Mortierella alpina* Δ 12-desaturase DNA, or which encode polypeptides which are substantially identical to the *Mortierella alpina* Δ 12-desaturase polypeptide, also can be used.

Other Desaturases

Encompassed by the present invention are related desaturases from the same or other organisms. Such related desaturases include variants of the disclosed Δ 6- or Δ 12-desaturase naturally occurring within the same or different species of *Mortierella*, as well as homologues of the disclosed Δ 6- or Δ 12-desaturase from other species. Also included are desaturases which, although

not substantially identical to the *Mortierella alpina* $\Delta 6$ - or $\Delta 12$ -desaturase, desaturate a fatty acid molecule at carbon 6 or 12, respectively, from the carboxyl end of a fatty acid molecule, or at carbon 12 or 6 from the terminal methyl carbon in an 18 carbon fatty acid molecule. Related desaturases can be identified by their ability to function substantially the same as the disclosed desaturases; that is, are still able to effectively convert LA to GLA, ALA to SDA or oleic acid to LA. Related desaturases also can be identified by screening sequence databases for sequences homologous to the disclosed desaturases, by hybridization of a probe based on the disclosed desaturases to a library constructed from the source organism, or by RT-PCR using mRNA from the source organism and primers based on the disclosed desaturases. Such desaturases include those from humans, *Dictyostelium discoideum* and *Phaeodactylum tricornutum*.

The regions of a desaturase polypeptide important for desaturase activity can be determined through routine mutagenesis, expression of the resulting mutant polypeptides and determination of their activities. Mutants may include deletions, insertions and point mutations, or combinations thereof. A typical functional analysis begins with deletion mutagenesis to determine the N- and C-terminal limits of the protein necessary for function, and then internal deletions, insertions or point mutants are made to further determine regions necessary for function. Other techniques such as cassette mutagenesis or total synthesis also can be used. Deletion mutagenesis is accomplished, for example, by using exonucleases to sequentially remove the 5' or 3' coding regions. Kits are available for such techniques. After deletion, the coding region is completed by ligating oligonucleotides containing start or stop codons to the deleted coding region after 5' or 3' deletion, respectively. Alternatively, oligonucleotides encoding start or stop codons are inserted into the coding region by a variety of methods including site-directed mutagenesis, mutagenic PCR or by ligation onto DNA digested at existing restriction sites. Internal deletions can similarly be made through a variety of methods including the use of existing restriction sites in the DNA, by use of mutagenic primers via site directed mutagenesis or mutagenic PCR. Insertions are made through methods such as linker-scanning

mutagenesis, site-directed mutagenesis or mutagenic PCR. Point mutations are made through techniques such as site-directed mutagenesis or mutagenic PCR.

Chemical mutagenesis also can be used for identifying regions of a desaturase polypeptide important for activity. A mutated construct is expressed, and the ability of the resulting altered protein to function as a desaturase is assayed. Such structure-function analysis can determine which regions may be deleted, which regions tolerate insertions, and which point mutations allow the mutant protein to function in substantially the same way as the native desaturase. All such mutant proteins and nucleotide sequences encoding them are within the scope of the present invention.

EXPRESSION OF DESATURASE GENES

Once the DNA encoding a desaturase polypeptide has been obtained, it is placed in a vector capable of replication in a host cell, or is propagated *in vitro* by means of techniques such as PCR or long PCR. Replicating vectors can include plasmids, phage, viruses, cosmids and the like. Desirable vectors include those useful for mutagenesis of the gene of interest or for expression of the gene of interest in host cells. The technique of long PCR has made *in vitro* propagation of large constructs possible, so that modifications to the gene of interest, such as mutagenesis or addition of expression signals, and propagation of the resulting constructs can occur entirely *in vitro* without the use of a replicating vector or a host cell.

For expression of a desaturase polypeptide, functional transcriptional and translational initiation and termination regions are operably linked to the DNA encoding the desaturase polypeptide. Expression of the polypeptide coding region can take place *in vitro* or in a host cell. Transcriptional and translational initiation and termination regions are derived from a variety of nonexclusive sources, including the DNA to be expressed, genes known or suspected to be capable of expression in the desired system, expression vectors, chemical synthesis, or from an endogenous locus in a host cell.

Expression In Vitro

In vitro expression can be accomplished, for example, by placing the coding region for the desaturase polypeptide in an expression vector designed for *in vitro* use and adding rabbit reticulocyte lysate and cofactors; labeled
5 amino acids can be incorporated if desired. Such *in vitro* expression vectors may provide some or all of the expression signals necessary in the system used. These methods are well known in the art and the components of the system are commercially available. The reaction mixture can then be assayed directly for the polypeptide, for example by determining its activity, or the synthesized
10 polypeptide can be purified and then assayed.

Expression In A Host Cell

Expression in a host cell can be accomplished in a transient or stable fashion. Transient expression can occur from introduced constructs which contain expression signals functional in the host cell, but which constructs do
15 not replicate and rarely integrate in the host cell, or where the host cell is not proliferating. Transient expression also can be accomplished by inducing the activity of a regulatable promoter operably linked to the gene of interest, although such inducible systems frequently exhibit a low basal level of expression. Stable expression can be achieved by introduction of a construct
20 that can integrate into the host genome or that autonomously replicates in the host cell. Stable expression of the gene of interest can be selected for through the use of a selectable marker located on or transfected with the expression construct, followed by selection for cells expressing the marker. When stable expression results from integration, integration of constructs can occur
25 randomly within the host genome or can be targeted through the use of constructs containing regions of homology with the host genome sufficient to target recombination with the host locus. Where constructs are targeted to an endogenous locus, all or some of the transcriptional and translational regulatory regions can be provided by the endogenous locus.

When increased expression of the desaturase polypeptide in the source organism is desired, several methods can be employed. Additional genes encoding the desaturase polypeptide can be introduced into the host organism. Expression from the native desaturase locus also can be increased through
5 homologous recombination, for example by inserting a stronger promoter into the host genome to cause increased expression, by removing destabilizing sequences from either the mRNA or the encoded protein by deleting that information from the host genome, or by adding stabilizing sequences to the mRNA (USPN 4,910,141).

10 When it is desirable to express more than one different gene, appropriate regulatory regions and expression methods, introduced genes can be propagated in the host cell through use of replicating vectors or by integration into the host genome. Where two or more genes are expressed from separate replicating vectors, it is desirable that each vector has a different means of replication.
15 Each introduced construct, whether integrated or not, should have a different means of selection and should lack homology to the other constructs to maintain stable expression and prevent reassortment of elements among constructs. Judicious choices of regulatory regions, selection means and method of propagation of the introduced construct can be experimentally determined so
20 that all introduced genes are expressed at the necessary levels to provide for synthesis of the desired products.

As an example, where the host cell is a yeast, transcriptional and translational regions functional in yeast cells are provided, particularly from the host species. The transcriptional initiation regulatory regions can be obtained,
25 for example from genes in the glycolytic pathway, such as alcohol dehydrogenase, glyceraldehyde-3-phosphate dehydrogenase (GPD), phosphoglucoisomerase, phosphoglycerate kinase, etc. or regulatable genes such as acid phosphatase, lactase, metallothionein, glucoamylase, etc. Any one of a number of regulatory sequences can be used in a particular situation,
30 depending upon whether constitutive or induced transcription is desired, the particular efficiency of the promoter in conjunction with the open-reading frame of interest, the ability to join a strong promoter with a control region from a

different promoter which allows for inducible transcription, ease of construction, and the like. Of particular interest are promoters which are activated in the presence of galactose. Galactose-inducible promoters (GAL1, GAL7, and GAL10) have been extensively utilized for high level and regulated expression of protein in yeast (Lue *et al.*, *Mol. Cell. Biol.* Vol. 7, p. 3446, 1987; Johnston, *Microbiol. Rev.* Vol. 51, p. 458, 1987). Transcription from the GAL promoters is activated by the GAL4 protein, which binds to the promoter region and activates transcription when galactose is present. In the absence of galactose, the antagonist GAL80 binds to GAL4 and prevents GAL4 from activating transcription. Addition of galactose prevents GAL80 from inhibiting activation by GAL4.

Nucleotide sequences surrounding the translational initiation codon ATG have been found to affect expression in yeast cells. If the desired polypeptide is poorly expressed in yeast, the nucleotide sequences of exogenous genes can be modified to include an efficient yeast translation initiation sequence to obtain optimal gene expression. For expression in *Saccharomyces*, this can be done by site-directed mutagenesis of an inefficiently expressed gene by fusing it in-frame to an endogenous *Saccharomyces* gene, preferably a highly expressed gene, such as the lactase gene.

The termination region can be derived from the 3' region of the gene from which the initiation region was obtained or from a different gene. A large number of termination regions are known to and have been found to be satisfactory in a variety of hosts from the same and different genera and species. The termination region usually is selected more as a matter of convenience rather than because of any particular property. Preferably, the termination region is derived from a yeast gene, particularly *Saccharomyces*, *Schizosaccharomyces*, *Candida* or *Kluyveromyces*. The 3' regions of two mammalian genes, γ interferon and $\alpha 2$ interferon, are also known to function in yeast.

INTRODUCTION OF CONSTRUCTS INTO HOST CELLS

Constructs comprising the gene of interest may be introduced into a host cell by standard techniques. These techniques include transformation, protoplast fusion, lipofection, transfection, transduction, conjugation, infection, bolistic impact, electroporation, microinjection, scraping, or any other method which introduces the gene of interest into the host cell. Methods of transformation which are used include lithium acetate transformation (*Methods in Enzymology*, Vol. 194, p. 186-187, 1991). For convenience, a host cell which has been manipulated by any method to take up a DNA sequence or construct will be referred to as "transformed" or "recombinant" herein.

The subject host will have at least have one copy of the expression construct and may have two or more, depending upon whether the gene is integrated into the genome, amplified, or is present on an extrachromosomal element having multiple copy numbers. Where the subject host is a yeast, four principal types of yeast plasmid vectors can be used: Yeast Integrating plasmids (YIps), Yeast Replicating plasmids (YRps), Yeast Centromere plasmids (YCps), and Yeast Episomal plasmids (YEps). YIps lack a yeast replication origin and must be propagated as integrated elements in the yeast genome. YRps have a chromosomally derived autonomously replicating sequence and are propagated as medium copy number (20 to 40), autonomously replicating, unstably segregating plasmids. YCps have both a replication origin and a centromere sequence and propagate as low copy number (10-20), autonomously replicating, stably segregating plasmids. YEps have an origin of replication from the yeast 2 μ m plasmid and are propagated as high copy number, autonomously replicating, irregularly segregating plasmids. The presence of the plasmids in yeast can be ensured by maintaining selection for a marker on the plasmid. Of particular interest are the yeast vectors pYES2 (a YEp plasmid available from Invitrogen, confers uracil prototrophy and a GAL1 galactose-inducible promoter for expression), pRS425-pG1 (a YEp plasmid obtained from Dr. T. H. Chang, Ass. Professor of Molecular Genetics, Ohio State University, containing a constitutive GPD promoter and conferring leucine prototrophy), and pYX424 (a YEp plasmid having a constitutive TP1 promoter and conferring

leucine prototrophy; Alber, T. and Kawasaki, G. (1982). *J. Mol. & Appl. Genetics* 1: 419).

The transformed host cell can be identified by selection for a marker contained on the introduced construct. Alternatively, a separate marker
5 construct may be introduced with the desired construct, as many transformation techniques introduce many DNA molecules into host cells. Typically, transformed hosts are selected for their ability to grow on selective media. Selective media may incorporate an antibiotic or lack a factor necessary for growth of the untransformed host, such as a nutrient or growth factor. An
10 introduced marker gene therefor may confer antibiotic resistance, or encode an essential growth factor or enzyme, and permit growth on selective media when expressed in the transformed host. Selection of a transformed host can also occur when the expressed marker protein can be detected, either directly or indirectly. The marker protein may be expressed alone or as a fusion to another
15 protein. The marker protein can be detected by its enzymatic activity; for example β galactosidase can convert the substrate X-gal to a colored product, and luciferase can convert luciferin to a light-emitting product. The marker protein can be detected by its light-producing or modifying characteristics; for example, the green fluorescent protein of *Aequorea victoria* fluoresces when
20 illuminated with blue light. Antibodies can be used to detect the marker protein or a molecular tag on, for example, a protein of interest. Cells expressing the marker protein or tag can be selected, for example, visually, or by techniques such as FACS or panning using antibodies. For selection of yeast transformants, any marker that functions in yeast may be used. Desirably,
25 resistance to kanamycin and the amino glycoside G418 are of interest, as well as ability to grow on media lacking uracil, leucine, lysine or tryptophan.

Of particular interest is the $\Delta 6$ - and $\Delta 12$ -desaturase-mediated production of PUFAs in prokaryotic and eukaryotic host cells. Prokaryotic cells of interest include *Eschericia*, *Bacillus*, *Lactobacillus*, *cyanobacteria* and the like.
30 Eukaryotic cells include mammalian cells such as those of lactating animals, avian cells such as of chickens, and other cells amenable to genetic manipulation including insect, fungal, and algae cells. The cells may be

cultured or formed as part or all of a host organism including an animal.

Viruses and bacteriophage also may be used with the cells in the production of PUFAs, particularly for gene transfer, cellular targeting and selection. In a preferred embodiment, the host is any microorganism or animal which produces and/or can assimilate exogenously supplied substrate(s) for a $\Delta 6$ - and/or $\Delta 12$ -desaturase, and preferably produces large amounts of one or more of the substrates. Examples of host animals include mice, rats, rabbits, chickens, quail, turkeys, bovines, sheep, pigs, goats, yaks, etc., which are amenable to genetic manipulation and cloning for rapid expansion of the transgene expressing population. For animals, the desaturase transgene(s) can be adapted for expression in target organelles, tissues and body fluids through modification of the gene regulatory regions. Of particular interest is the production of PUFAs in the breast milk of the host animal.

Expression In Yeast

Examples of host microorganisms include *Saccharomyces cerevisiae*, *Saccharomyces carlsbergensis*, or other yeast such as *Candida*, *Kluyveromyces* or other fungi, for example, filamentous fungi such as *Aspergillus*, *Neurospora*, *Penicillium*, etc. Desirable characteristics of a host microorganism are, for example, that it is genetically well characterized, can be used for high level expression of the product using ultra-high density fermentation, and is on the GRAS (generally recognized as safe) list since the proposed end product is intended for ingestion by humans. Of particular interest is use of a yeast, more particularly baker's yeast (*S. cerevisiae*), as a cell host in the subject invention. Strains of particular interest are SC334 (Mat α pep4-3 prb1-1122 ura3-52 leu2-3, 112 reg1-501 gal1; *Gene* 83:57-64, 1989, Hovland P. *et al.*), YTC34 (α ade2-101 his3 Δ 200 lys2-801 ura3-52; obtained from Dr. T. H. Chang, Ass. Professor of Molecular Genetics, Ohio State University), YTC41 (α/α ura3-52/ura3=52 lys2-801/lys2-801 ade2-101/ade2-101 trp1- Δ 1/trp1- Δ 1 his3 Δ 200/his3 Δ 200 leu2 Δ 1/leu2 Δ 1; obtained from Dr. T. H. Chang, Ass. Professor of Molecular Genetics, Ohio State University), BJ1995 (obtained from the Yeast Genetic

Stock Centre, 1021 Donner Laboratory, Berkeley, CA 94720), INVSC1 (Mat α hiw3 Δ 1 leu2 trp1-289 ura3-52; obtained from Invitrogen, 1600 Faraday Ave., Carlsbad, CA 92008) and INVSC2 (Mat α his3 Δ 200 ura3-167; obtained from Invitrogen).

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Expression in Avian Species

For producing PUFAs in avian species and cells, such as chickens, turkeys, quail and ducks, gene transfer can be performed by introducing a nucleic acid sequence encoding a Δ 6 and/or Δ 12-desaturase into the cells following procedures known in the art. If a transgenic animal is desired, pluripotent stem cells of embryos can be provided with a vector carrying a desaturase encoding transgene and developed into adult animal (USPN 5,162,215; Ono *et al.* (1996) *Comparative Biochemistry and Physiology A* 113(3):287-292; WO 9612793; WO 9606160). In most cases, the transgene will be modified to express high levels of the desaturase in order to increase production of PUFAs. The transgene can be modified, for example, by providing transcriptional and/or translational regulatory regions that function in avian cells, such as promoters which direct expression in particular tissues and egg parts such as yolk. The gene regulatory regions can be obtained from a variety of sources, including chicken anemia or avian leukosis viruses or avian genes such as a chicken ovalbumin gene.

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Expression in Insect Cells

Production of PUFAs in insect cells can be conducted using baculovirus expression vectors harboring one or more desaturase transgenes. Baculovirus expression vectors are available from several commercial sources such as Clontech. Methods for producing hybrid and transgenic strains of algae, such as marine algae, which contain and express a desaturase transgene also are provided. For example, transgenic marine algae may be prepared as described in USPN 5,426,040. As with the other expression systems described above, the timing, extent of expression and activity of the desaturase transgene can be

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regulated by fitting the polypeptide coding sequence with the appropriate transcriptional and translational regulatory regions selected for a particular use. Of particular interest are promoter regions which can be induced under preselected growth conditions. For example, introduction of temperature
5 sensitive and/or metabolite responsive mutations into the desaturase transgene coding sequences, its regulatory regions, and/or the genome of cells into which the transgene is introduced can be used for this purpose.

The transformed host cell is grown under appropriate conditions adapted for a desired end result. For host cells grown in culture, the conditions are
10 typically optimized to produce the greatest or most economical yield of PUFAs, which relates to the selected desaturase activity. Media conditions which may be optimized include: carbon source, nitrogen source, addition of substrate, final concentration of added substrate, form of substrate added, aerobic or anaerobic growth, growth temperature, inducing agent, induction temperature,
15 growth phase at induction, growth phase at harvest, pH, density, and maintenance of selection. Microorganisms of interest, such as yeast are preferably grown in selected medium. For yeast, complex media such as peptone broth (YPD) or a defined media such as a minimal media (contains amino acids, yeast nitrogen base, and ammonium sulfate, and lacks a
20 component for selection, for example uracil) are preferred. Desirably, substrates to be added are first dissolved in ethanol. Where necessary, expression of the polypeptide of interest may be induced, for example by including or adding galactose to induce expression from a GAL promoter.

Expression In Plants

25 Production of PUFA's in plants can be conducted using various plant transformation systems such as the use of *Agrobacterium tumefaciens*, plant viruses, particle cell transformation and the like which are disclosed in Applicant's related applications U.S. Application Serial Nos. 08/834,033 and 08/956,985 and continuation-in-part applications filed simultaneously with this
30 application all of which are hereby incorporated by reference.

Expression In An Animal

Expression in cells of a host animal can likewise be accomplished in a transient or stable manner. Transient expression can be accomplished via known methods, for example infection or lipofection, and can be repeated in order to maintain desired expression levels of the introduced construct (*see* Ebert, PCT publication WO 94/05782). Stable expression can be accomplished via integration of a construct into the host genome, resulting in a transgenic animal. The construct can be introduced, for example, by microinjection of the construct into the pronuclei of a fertilized egg, or by transfection, retroviral infection or other techniques whereby the construct is introduced into a cell line which may form or be incorporated into an adult animal (U.S. Patent No. 4,873,191; U.S. Patent No. 5,530,177; U.S. Patent No. 5,565,362; U.S. Patent No. 5,366,894; Willmut *et al* (1997) Nature 385:810). The recombinant eggs or embryos are transferred to a surrogate mother (U.S. Patent No. 4,873,191; U.S. Patent No. 5,530,177; U.S. Patent No. 5,565,362; U.S. Patent No. 5,366,894; Wilmut *et al* (*supra*)).

After birth, transgenic animals are identified, for example, by the presence of an introduced marker gene, such as for coat color, or by PCR or Southern blotting from a blood, milk or tissue sample to detect the introduced construct, or by an immunological or enzymological assay to detect the expressed protein or the products produced therefrom (U.S. Patent No. 4,873,191; U.S. Patent No. 5,530,177; U.S. Patent No. 5,565,362; U.S. Patent No. 5,366,894; Wilmut *et al* (*supra*)). The resulting transgenic animals may be entirely transgenic or may be mosaics, having the transgenes in only a subset of their cells. The advent of mammalian cloning, accomplished by fusing a nucleated cell with an enucleated egg, followed by transfer into a surrogate mother, presents the possibility of rapid, large-scale production upon obtaining a "founder" animal or cell comprising the introduced construct; prior to this, it was necessary for the transgene to be present in the germ line of the animal for propagation (Wilmut *et al* (*supra*)).

Expression in a host animal presents certain efficiencies, particularly where the host is a domesticated animal. For production of PUFAs in a fluid readily obtainable from the host animal, such as milk, the desaturase transgene can be expressed in mammary cells from a female host, and the PUFA content of the host cells altered. The desaturase transgene can be adapted for expression so that it is retained in the mammary cells, or secreted into milk, to form the PUFA reaction products localized to the milk (PCT publication WO 95/24488). Expression can be targeted for expression in mammary tissue using specific regulatory sequences, such as those of bovine α -lactalbumin, α -casein, β -casein, γ -casein, κ -casein, β -lactoglobulin, or whey acidic protein, and may optionally include one or more introns and/or secretory signal sequences (U.S. Patent No. 5,530,177; Rosen, U.S. Patent No. 5,565,362; Clark *et al.*, U.S. Patent No. 5,366,894; Garner *et al.*, PCT publication WO 95/23868). Expression of desaturase transgenes, or antisense desaturase transcripts, adapted in this manner can be used to alter the levels of specific PUFAs, or derivatives thereof, found in the animals milk. Additionally, the desaturase transgene(s) can be expressed either by itself or with other transgenes, in order to produce animal milk containing higher proportions of desired PUFAs or PUFA ratios and concentrations that resemble human breast milk (Prieto *et al.*, PCT publication WO 95/24494).

PURIFICATION OF FATTY ACIDS

The desaturated fatty acids may be found in the host microorganism or animal as free fatty acids or in conjugated forms such as acylglycerols, phospholipids, sulfolipids or glycolipids, and may be extracted from the host cell through a variety of means well-known in the art. Such means may include extraction with organic solvents, sonication, supercritical fluid extraction using for example carbon dioxide, and physical means such as presses, or combinations thereof. Of particular interest is extraction with hexane or methanol and chloroform. Where desirable, the aqueous layer can be acidified to protonate negatively charged moieties and thereby increase partitioning of desired products into the organic layer. After extraction, the organic solvents can be removed by evaporation under a stream of nitrogen. When isolated in

detectable reaction products, magnetic molecules, fluorescent molecules or molecules whose fluorescence or light-emitting characteristics change upon binding. Examples of labelling methods can be found in USPN 5,011,770. Alternatively, the binding of target molecules can be directly detected by measuring the change in heat of solution on binding of probe to target via isothermal titration calorimetry, or by coating the probe or target on a surface and detecting the change in scattering of light from the surface produced by binding of target or probe, respectively, as may be done with the BIAcore system.

PUFAs produced by recombinant means find applications in a wide variety of areas. Supplementation of animals or humans with PUFAs in various forms can result in increased levels not only of the added PUFAs but of their metabolic progeny as well.

NUTRITIONAL COMPOSITIONS

The present invention also includes nutritional compositions. Such compositions, for purposes of the present invention, include any food or preparation for human consumption including for enteral or parenteral consumption, which when taken into the body (a) serve to nourish or build up tissues or supply energy and/or (b) maintain, restore or support adequate nutritional status or metabolic function.

The nutritional composition of the present invention comprises at least one oil or acid produced in accordance with the present invention and may either be in a solid or liquid form. Additionally, the composition may include edible macronutrients, vitamins and minerals in amounts desired for a particular use. The amount of such ingredients will vary depending on whether the composition is intended for use with normal, healthy infants, children or adults having specialized needs such as those which accompany certain metabolic conditions (e.g., metabolic disorders).

Examples of macronutrients which may be added to the composition include but are not limited to edible fats, carbohydrates and proteins. Examples of such edible fats include but are not limited to coconut oil, soy oil, and mono-

and diglycerides. Examples of such carbohydrates include but are not limited to glucose, edible lactose and hydrolyzed starch. Additionally, examples of proteins which may be utilized in the nutritional composition of the invention include but are not limited to soy proteins, electrodialysed whey ,
5 electrodialysed skim milk, milk whey, or the hydrolysates of these proteins.

With respect to vitamins and minerals, the following may be added to the nutritional compositions of the present invention: calcium, phosphorus, potassium, sodium, chloride, magnesium, manganese, iron, copper, zinc, selenium, iodine, and Vitamins A, E, D, C, and the B complex. Other such
10 vitamins and minerals may also be added.

The components utilized in the nutritional compositions of the present invention will be of semi-purified or purified origin. By semi-purified or purified is meant a material which has been prepared by purification of a natural material or by synthesis.

15 Examples of nutritional compositions of the present invention include but are not limited to infant formulas, dietary supplements, and rehydration compositions. Nutritional compositions of particular interest include but are not limited to those utilized for enteral and parenteral supplementation for infants, specialist infant formulae, supplements for the elderly, and supplements for
20 those with gastrointestinal difficulties and/or malabsorption.

Nutritional Compositions

A typical nutritional composition of the present invention will contain edible macronutrients, vitamins and minerals in amounts desired for a particular use. The amounts of such ingredients will vary depending on whether the
25 formulation is intended for use with normal, healthy individuals temporarily exposed to stress, or to subjects having specialized needs due to certain chronic or acute disease states (e.g., metabolic disorders). It will be understood by persons skilled in the art that the components utilized in a nutritional formulation of the present invention are of semi-purified or purified origin. By
30 semi-purified or purified is meant a material that has been prepared by

purification of a natural material or by synthesis. These techniques are well known in the art (See, e.g., Code of Federal Regulations for Food Ingredients and Food Processing; Recommended Dietary Allowances, 10th Ed., National Academy Press, Washington, D.C., 1989).

5 In a preferred embodiment, a nutritional formulation of the present invention is an enteral nutritional product, more preferably an adult or child enteral nutritional product. Accordingly in a further aspect of the invention, a nutritional formulation is provided that is suitable for feeding adults or children, who are experiencing stress. The formula comprises, in addition to the PUFAs
10 of the invention; macronutrients, vitamins and minerals in amounts designed to provide the daily nutritional requirements of adults.

The macronutritional components include edible fats, carbohydrates and proteins. Exemplary edible fats are coconut oil, soy oil, and mono- and diglycerides and the PUFA oils of this invention. Exemplary carbohydrates are
15 glucose, edible lactose and hydrolyzed cornstarch. A typical protein source would be soy protein, electrodialysed whey or electrodialysed skim milk or milk whey, or the hydrolysates of these proteins, although other protein sources are also available and may be used. These macronutrients would be added in the form of commonly accepted nutritional compounds in amount equivalent to
20 those present in human milk or an energy basis, i.e., on a per calorie basis.

Methods for formulating liquid and enteral nutritional formulas are well known in the art and are described in detail in the examples.

The enteral formula can be sterilized and subsequently utilized on a ready-to-feed (RTF) basis or stored in a concentrated liquid or a powder. The
25 powder can be prepared by spray drying the enteral formula prepared as indicated above, and the formula can be reconstituted by rehydrating the concentrate. Adult and infant nutritional formulas are well known in the art and commercially available (e.g., Similac®, Ensure®, Jevity® and Alimentum® from Ross Products Division, Abbott Laboratories). An oil or acid of the
30 present invention can be added to any of these formulas in the amounts described below.

The energy density of the nutritional composition when in liquid form, can typically range from about 0.6 to 3.0 Kcal per ml. When in solid or powdered form, the nutritional supplement can contain from about 1.2 to more than 9 Kcals per gm, preferably 3 to 7 Kcals per gm. In general, the osmolality of a liquid product should be less than 700 mOsm and more preferably less than 660 mOsm.

The nutritional formula would typically include vitamins and minerals, in addition to the PUFAs of the invention, in order to help the individual ingest the minimum daily requirements for these substances. In addition to the PUFAs listed above, it may also be desirable to supplement the nutritional composition with zinc, copper, and folic acid in addition to antioxidants. It is believed that these substances will also provide a boost to the stressed immune system and thus will provide further benefits to the individual. The presence of zinc, copper or folic acid is optional and is not required in order to gain the beneficial effects on immune suppression. Likewise a pharmaceutical composition can be supplemented with these same substances as well.

In a more preferred embodiment, the nutritional contains, in addition to the antioxidant system and the PUFA component, a source of carbohydrate wherein at least 5 weight % of said carbohydrate is an indigestible oligosaccharide. In yet a more preferred embodiment, the nutritional composition additionally contains protein, taurine and carnitine.

The PUFAs, or derivatives thereof, made by the disclosed method can be used as dietary substitutes, or supplements, particularly infant formulas, for patients undergoing intravenous feeding or for preventing or treating malnutrition. Typically, human breast milk has a fatty acid profile comprising from about 0.15 % to about 0.36 % as DHA, from about 0.03 % to about 0.13 % as EPA, from about 0.30 % to about 0.88 % as ARA, from about 0.22 % to about 0.67 % as DGLA, and from about 0.27 % to about 1.04 % as GLA. Additionally, the predominant triglyceride in human milk has been reported to be 1,3-di-oleoyl-2-palmitoyl, with 2-palmitoyl glycerides reported as better absorbed than 2-oleoyl or 2-lineoyl glycerides (USPN 4,876,107). Thus, fatty acids such as ARA, DGLA, GLA and/or EPA produced by the invention can be

used to alter the composition of infant formulas to better replicate the PUFA composition of human breast milk. In particular, an oil composition for use in a pharmacologic or food supplement, particularly a breast milk substitute or supplement, will preferably comprise one or more of ARA, DGLA and GLA.

5 More preferably the oil will comprise from about 0.3 to 30% ARA, from about 0.2 to 30% DGLA, and from about 0.2 to about 30% GLA.

In addition to the concentration, the ratios of ARA, DGLA and GLA can be adapted for a particular given end use. When formulated as a breast milk supplement or substitute, an oil composition which contains two or more of

10 ARA, DGLA and GLA will be provided in a ratio of about 1:19:30 to about 6:1:0.2, respectively. For example, the breast milk of animals can vary in ratios of ARA:DGLA:DGL ranging from 1:19:30 to 6:1:0.2, which includes intermediate ratios which are preferably about 1:1:1, 1:2:1, 1:1:4. When produced together in a host cell, adjusting the rate and percent of conversion of

15 a precursor substrate such as GLA and DGLA to ARA can be used to precisely control the PUFA ratios. For example, a 5% to 10% conversion rate of DGLA to ARA can be used to produce an ARA to DGLA ratio of about 1:19, whereas a conversion rate of about 75% to 80% can be used to produce an ARA to DGLA ratio of about 6:1. Therefore, whether in a cell culture system or in a

20 host animal, regulating the timing, extent and specificity of desaturase expression as described can be used to modulate the PUFA levels and ratios. Depending on the expression system used, e.g., cell culture or an animal expressing oil(s) in its milk, the oils also can be isolated and recombined in the desired concentrations and ratios. Amounts of oils providing these ratios of

25 PUFA can be determined following standard protocols. PUFAs, or host cells containing them, also can be used as animal food supplements to alter an animal's tissue or milk fatty acid composition to one more desirable for human or animal consumption.

For dietary supplementation, the purified PUFAs, or derivatives thereof,

30 may be incorporated into cooking oils, fats or margarines formulated so that in normal use the recipient would receive the desired amount. The PUFAs may

also be incorporated into infant formulas, nutritional supplements or other food products, and may find use as anti-inflammatory or cholesterol lowering agents.

Pharmaceutical Compositions

5 The present invention also encompasses a pharmaceutical composition comprising one or more of the acids and/or resulting oils produced in accordance with the methods described herein. More specifically, such a pharmaceutical composition may comprise one or more of the acids and/or oils as well as a standard, well-known, non-toxic pharmaceutically acceptable carrier, adjuvant or vehicle such as, for example, phosphate buffered saline, 10 water, ethanol, polyols, vegetable oils, a wetting agent or an emulsion such as a water/oil emulsion. The composition may be in either a liquid or solid form. For example, the composition may be in the form of a tablet, capsule, ingestible liquid or powder, injectible, or topical ointment or cream.

15 Possible routes of administration include, for example, oral, rectal and parenteral. The route of administration will, of course, depend upon the desired effect. For example, if the composition is being utilized to treat rough, dry, or aging skin, to treat injured or burned skin, or to treat skin or hair affected by a disease or condition, it may perhaps be applied topically.

20 The dosage of the composition to be administered to the patient may be determined by one of ordinary skill in the art and depends upon various factors such as weight of the patient, age of the patient, immune status of the patient, etc.

25 With respect to form, the composition may be, for example, a solution, a dispersion, a suspension, an emulsion or a sterile powder which is then reconstituted.

Additionally, the composition of the present invention may be utilized for cosmetic purposes. It may be added to pre-existing cosmetic compositions such that a mixture is formed or may be used as a sole composition.

Pharmaceutical compositions may be utilized to administer the PUFA component to an individual. Suitable pharmaceutical compositions may comprise physiologically acceptable sterile aqueous or non-aqueous solutions, dispersions, suspensions or emulsions and sterile powders for reconstitution into sterile solutions or dispersions for ingestion. Examples of suitable aqueous and non-aqueous carriers, diluents, solvents or vehicles include water, ethanol, polyols (propyleneglycol, polyethyleneglycol, glycerol, and the like), suitable mixtures thereof, vegetable oils (such as olive oil) and injectable organic esters such as ethyl oleate. Proper fluidity can be maintained, for example, by the maintenance of the required particle size in the case of dispersions and by the use of surfactants. It may also be desirable to include isotonic agents, for example sugars, sodium chloride and the like. Besides such inert diluents, the composition can also include adjuvants, such as wetting agents, emulsifying and suspending agents, sweetening, flavoring and perfuming agents.

Suspensions, in addition to the active compounds, may contain suspending agents, as for example, ethoxylated isostearyl alcohols, polyoxyethylene sorbitol and sorbitan esters, microcrystalline cellulose, aluminum metahydroxide, bentonite, agar-agar and tragacanth or mixtures of these substances, and the like.

Solid dosage forms such as tablets and capsules can be prepared using techniques well known in the art. For example, PUFAs of the invention can be tableted with conventional tablet bases such as lactose, sucrose, and cornstarch in combination with binders such as acacia, cornstarch or gelatin, disintegrating agents such as potato starch or alginic acid and a lubricant such as stearic acid or magnesium stearate. Capsules can be prepared by incorporating these excipients into a gelatin capsule along with the antioxidants and the PUFA component. The amount of the antioxidants and PUFA component that should be incorporated into the pharmaceutical formulation should fit within the guidelines discussed above.

As used in this application, the term "treat" refers to either preventing, or reducing the incidence of, the undesired occurrence. For example, to treat immune suppression refers to either preventing the occurrence of this

suppression or reducing the amount of such suppression. The terms "patient" and "individual" are being used interchangeably and both refer to an animal. The term "animal" as used in this application refers to any warm-blooded mammal including, but not limited to, dogs, humans, monkeys, and apes. As
5 used in the application the term "about" refers to an amount varying from the stated range or number by a reasonable amount depending upon the context of use. Any numerical number or range specified in the specification should be considered to be modified by the term about.

"Dose" and "serving" are used interchangeably and refer to the amount
10 of the nutritional or pharmaceutical composition ingested by the patient in a single setting and designed to deliver effective amounts of the antioxidants and the structured triglyceride. As will be readily apparent to those skilled in the art, a single dose or serving of the liquid nutritional powder should supply the amount of antioxidants and PUFAs discussed above. The amount of the dose or
15 serving should be a volume that a typical adult can consume in one sitting. This amount can vary widely depending upon the age, weight, sex or medical condition of the patient. However as a general guideline, a single serving or dose of a liquid nutritional produce should be considered as encompassing a volume from 100 to 600 ml, more preferably from 125 to 500 ml and most
20 preferably from 125 to 300 ml.

The PUFAs of the present invention may also be added to food even when supplementation of the diet is not required. For example, the composition may be added to food of any type including but not limited to margarines, modified butters, cheeses, milk, yogurt, chocolate, candy, snacks, salad oils,
25 cooking oils, cooking fats, meats, fish and beverages.

Pharmaceutical Applications

For pharmaceutical use (human or veterinary), the compositions are generally administered orally but can be administered by any route by which they may be successfully absorbed, e.g., parenterally (i.e. subcutaneously,
30 intramuscularly or intravenously), rectally or vaginally or topically, for example, as a skin ointment or lotion. The PUFAs of the present invention may

be administered alone or in combination with a pharmaceutically acceptable carrier or excipient. Where available, gelatin capsules are the preferred form of oral administration. Dietary supplementation as set forth above also can provide an oral route of administration. The unsaturated acids of the present invention may be administered in conjugated forms, or as salts, esters, amides or prodrugs of the fatty acids. Any pharmaceutically acceptable salt is encompassed by the present invention; especially preferred are the sodium, potassium or lithium salts. Also encompassed are the N-alkylpolyhydroxamine salts, such as N-methyl glucamine, found in PCT publication WO 96/33155. The preferred esters are the ethyl esters. As solid salts, the PUFAs also can be administered in tablet form. For intravenous administration, the PUFAs or derivatives thereof may be incorporated into commercial formulations such as Intralipids. The typical normal adult plasma fatty acid profile comprises 6.64 to 9.46% of ARA, 1.45 to 3.11% of DGLA, and 0.02 to 0.08% of GLA. These PUFAs or their metabolic precursors can be administered, either alone or in mixtures with other PUFAs, to achieve a normal fatty acid profile in a patient. Where desired, the individual components of formulations may be individually provided in kit form, for single or multiple use. A typical dosage of a particular fatty acid is from 0.1 mg to 20 g, or even 100 g daily, and is preferably from 10 mg to 1, 2, 5 or 10 g daily as required, or molar equivalent amounts of derivative forms thereof. Parenteral nutrition compositions comprising from about 2 to about 30 weight percent fatty acids calculated as triglycerides are encompassed by the present invention; preferred is a composition having from about 1 to about 25 weight percent of the total PUFA composition as GLA (USPN 5,196,198). Other vitamins, and particularly fat-soluble vitamins such as vitamin A, D, E and L-carnitine can optionally be included. Where desired, a preservative such as α tocopherol may be added, typically at about 0.1% by weight.

Suitable pharmaceutical compositions may comprise physiologically acceptable sterile aqueous or non-aqueous solutions, dispersions, suspensions or emulsions and sterile powders for reconstitution into sterile injectible solutions or dispersions. Examples of suitable aqueous and non-aqueous carriers,

diluents, solvents or vehicles include water, ethanol, polyols (propyleneglycol, polyethyleneglycol, glycerol, and the like), suitable mixtures thereof, vegetable oils (such as olive oil) and injectable organic esters such as ethyl oleate. Proper fluidity can be maintained, for example, by the maintenance of the required particle size in the case of dispersions and by the use of surfactants. It may also be desirable to include isotonic agents, for example sugars, sodium chloride and the like. Besides such inert diluents, the composition can also include adjuvants, such as wetting agents, emulsifying and suspending agents, sweetening, flavoring and perfuming agents.

Suspensions in addition to the active compounds, may contain suspending agents, as for example, ethoxylated isostearyl alcohols, polyoxyethylene sorbitol and sorbitan esters, microcrystalline cellulose, aluminum metahydroxide, bentonite, agar-agar and tragacanth, or mixtures of these substances and the like.

An especially preferred pharmaceutical composition contains diacetyltartaric acid esters of mono- and diglycerides dissolved in an aqueous medium or solvent. Diacetyltartaric acid esters of mono- and diglycerides have an HLB value of about 9-12 and are significantly more hydrophilic than existing antimicrobial lipids that have HLB values of 2-4. Those existing hydrophobic lipids cannot be formulated into aqueous compositions. As disclosed herein, those lipids can now be solubilized into aqueous media in combination with diacetyltartaric acid esters of mono- and diglycerides. In accordance with this embodiment, diacetyltartaric acid esters of mono- and diglycerides (e.g., DATEM-C12:0) is melted with other active antimicrobial lipids (e.g., 18:2 and 12:0 monoglycerides) and mixed to obtain a homogeneous mixture. Homogeneity allows for increased antimicrobial activity. The mixture can be completely dispersed in water. This is not possible without the addition of diacetyltartaric acid esters of mono- and diglycerides and premixing with other monoglycerides prior to introduction into water. The aqueous composition can then be admixed under sterile conditions with physiologically acceptable diluents, preservatives, buffers or propellants as may be required to form a spray or inhalant.

The present invention also encompasses the treatment of numerous disorders with fatty acids. Supplementation with PUFAs of the present invention can be used to treat restenosis after angioplasty. Symptoms of inflammation, rheumatoid arthritis, and asthma and psoriasis can be treated with the PUFAs of the present invention. Evidence indicates that PUFAs may be involved in calcium metabolism, suggesting that PUFAs of the present invention may be used in the treatment or prevention of osteoporosis and of kidney or urinary tract stones.

The PUFAs of the present invention can be used in the treatment of cancer. Malignant cells have been shown to have altered fatty acid compositions; addition of fatty acids has been shown to slow their growth and cause cell death, and to increase their susceptibility to chemotherapeutic agents. GLA has been shown to cause reexpression on cancer cells of the E-cadherin cellular adhesion molecules, loss of which is associated with aggressive metastasis. Clinical testing of intravenous administration of the water soluble lithium salt of GLA to pancreatic cancer patients produced statistically significant increases in their survival. PUFA supplementation may also be useful for treating cachexia associated with cancer.

The PUFAs of the present invention can also be used to treat diabetes (USPN 4,826,877; Horrobin *et al.*, Am. J. Clin. Nutr. Vol. 57 (Suppl.), 732S-737S). Altered fatty acid metabolism and composition has been demonstrated in diabetic animals. These alterations have been suggested to be involved in some of the long-term complications resulting from diabetes, including retinopathy, neuropathy, nephropathy and reproductive system damage. Primrose oil, which contains GLA, has been shown to prevent and reverse diabetic nerve damage.

The PUFAs of the present invention can be used to treat eczema, reduce blood pressure and improve math scores. Essential fatty acid deficiency has been suggested as being involved in eczema, and studies have shown beneficial effects on eczema from treatment with GLA. GLA has also been shown to reduce increases in blood pressure associated with stress, and to improve performance on arithmetic tests. GLA and DGLA have been shown to inhibit

platelet aggregation, cause vasodilation, lower cholesterol levels and inhibit proliferation of vessel wall smooth muscle and fibrous tissue (Brenner *et al.*, Adv. Exp. Med. Biol. Vol. 83, p. 85-101, 1976). Administration of GLA or DGLA, alone or in combination with EPA, has been shown to reduce or prevent gastro-intestinal bleeding and other side effects caused by non-steroidal anti-inflammatory drugs (USPN 4,666,701). GLA and DGLA have also been shown to prevent or treat endometriosis and premenstrual syndrome (USPN 4,758,592) and to treat myalgic encephalomyelitis and chronic fatigue after viral infections (USPN 5,116,871).

Further uses of the PUFAs of this invention include use in treatment of AIDS, multiple sclerosis, acute respiratory syndrome, hypertension and inflammatory skin disorders. The PUFAs of the inventions also can be used for formulas for general health as well as for geriatric treatments.

Veterinary Applications

It should be noted that the above-described pharmaceutical and nutritional compositions may be utilized in connection with animals, as well as humans, as animals experience many of the same needs and conditions as human. For example, the oil or acids of the present invention may be utilized in animal feed supplements.

The following examples are presented by way of illustration, not of limitation.

Examples

Example 1 Construction of a cDNA Library from *Mortierella alpina*

Example 2 Isolation of a $\Delta 6$ -desaturase Nucleotide Sequence from *Mortierella alpina*

Example 3 Identification of $\Delta 6$ -desaturases Homologous to the *Mortierella alpina* $\Delta 6$ -desaturase

Example 4 Isolation of a $\Delta 12$ -desaturase Nucleotide Sequence from *Mortierella Alpina*

- Example 5 Expression of *M. alpina* Desaturase Clones in Baker's Yeast
- Example 6 Initial Optimization of Culture Conditions
- Example 7 Distribution of PUFAs in Yeast Lipid Fractions
- 5 Example 8 Further Culture Optimization and Coexpression of $\Delta 6$ and $\Delta 12$ -desaturases
- Example 9 Identification of Homologues to *M. alpina* $\Delta 5$ and $\Delta 6$ desaturases
- 10 Example 10 Identification of *M. alpina* $\Delta 5$ and $\Delta 6$ homologues in other PUFA-producing organisms
- Example 11 Identification of *M. alpina* $\Delta 5$ and $\Delta 6$ homologues in other PUFA-producing organisms
- Example 12 Human Desaturase Gene Sequences
- 15 Example 13 Nutritional Compositions

Example 1

Construction of a cDNA Library from *Mortierella alpina*

Total RNA was isolated from a 3 day old PUFA-producing culture of *Mortierella alpina* using the protocol of Hoge *et al.* (1982) *Experimental Mycology* 6:225-232. The RNA was used to prepare double-stranded cDNA using BRL's lambda-ZipLox system following the manufactures instructions. Several size fractions of the *M. alpina* cDNA were packaged separately to yield libraries with different average-sized inserts. A "full-length" library contains approximately 3×10^6 clones with an average insert size of 1.77 kb. The

20

25 "sequencing-grade" library contains approximately 6×10^5 clones with an average insert size of 1.1 kb.

Example 2

Isolation of a $\Delta 6$ -desaturase Nucleotide Sequence from *Mortierella Alpina*

A nucleic acid sequence from a partial cDNA clone, Ma524, encoding a $\Delta 6$ fatty acid desaturase from *Mortierella alpina* was obtained by random
5 sequencing of clones from the *M. alpina* cDNA sequencing grade library described in Example 1. cDNA-containing plasmids were excised as follows:

Five μ l of phage were combined with 100 μ l of *E. coli* DH10B(ZIP) grown in ECLB plus 10 μ g/ml kanamycin, 0.2% maltose, and 10 mM $MgSO_4$ and incubated at 37 degrees for 15 minutes. 0.9 ml SOC was added and 100 μ l
10 of the bacteria immediately plated on each of 10 ECLB + 50 μ g Pen plates. No 45 minute recovery time was needed. The plates were incubated overnight at 37°. Colonies were picked into ECLB + 50 μ g Pen media for overnight cultures to be used for making glycerol stocks and miniprep DNA. An aliquot of the culture used for the miniprep is stored as a glycerol stock. Plating on ECLB +
15 50 μ g Pen/ml resulted in more colonies and a greater proportion of colonies containing inserts than plating on 100 μ g/ml Pen.

Random colonies were picked and plasmid DNA purified using Qiagen miniprep kits. DNA sequence was obtained from the 5' end of the cDNA insert and compared to the National Center for Biotechnology Information (NCBI)
20 nonredundant database using the BLASTX algorithm. Ma524 was identified as a putative desaturase based on DNA sequence homology to previously identified desaturases.

A full-length cDNA clone was isolated from the *M. alpina* full-length library and designed pCGN5532. The cDNA is contained as a 1617 bp insert in
25 the vector pZL1 (BRL) and, beginning with the first ATG, contains an open reading frame encoding 457 amino acids. The three conserved "histidine boxes" known to be conserved among membrane-bound deaturases (Okuley, et al. (1994) *The Plant Cell* 6:147-158) were found to be present at amino acid positions 172-176, 209-213, and 395-399 (see Figure 3). As with other

membrane-bound $\Delta 6$ -desaturases the final HXXHH histidine box motif was found to be QXXHH. The amino acid sequence of Ma524 was found to display significant homology to a portion of a *Caenorhabditis elegans* cosmid, WO6D2.4, a cytochrome b5/desaturase fusion protein from sunflower, and the
5 *Synechocystis* and *Spirulina* $\Delta 6$ -desaturases. In addition, Ma524 was shown to have homology to the borage $\Delta 6$ -desaturase amino sequence (PCT publication W) 96/21022). Ma524 thus appears to encode a $\Delta 6$ -desaturase that is related to the borage and algal $\Delta 6$ -desaturases. The peptide sequences are shown as SEQ ID NO:5 - SEQ ID NO:11.

10 The amino terminus of the encoded protein was found to exhibit significant homology to cytochrome b5 proteins. The *Mortierella* cDNA clone appears to represent a fusion between a cytochrome b5 and a fatty acid desaturase. Since cytochrome b5 is believed to function as the electron donor for membrane-bound desaturase enzymes, it is possible that the N-terminal
15 cytochrome b5 domain of this desaturase protein is involved in its function. This may be advantageous when expressing the desaturase in heterologous systems for PUFA production. However, it should be noted that, although the amino acid sequences of Ma524 and the borage $\Delta 6$ were found to contain regions of homology, the base compositions of the cDNAs were shown to be
20 significantly different. For example, the borage cDNA was shown to have an overall base composition of 60 % A/T, with some regions exceeding 70 %, while Ma524 was shown to have an average of 44 % A/T base composition, with no regions exceeding 60 %. This may have implications for expressing the cDNAs in microorganisms or animals which favor different base compositions.
25 It is known that poor expression of recombinant genes can occur when the host prefers a base composition different from that of the introduced gene. Mechanisms for such poor expression include decreased stability, cryptic splice sites, and/or translatability of the mRNA and the like.

Example 3Identification of $\Delta 6$ -desaturases Homologous to the
Mortierella alpina $\Delta 6$ -desaturase

Nucleic acid sequences that encode putative $\Delta 6$ -desaturases were identified through a BLASTX search of the Expressed Sequence Tag ("EST") databases through NCBI using the Ma524 amino acid sequence. Several sequences showed significant homology. In particular, the deduced amino acid sequence of two *Arabidopsis thaliana* sequences, (accession numbers F13728 and T42806) showed homology to two different regions of the deduced amino acid sequence of Ma524. The following PCR primers were designed:

ATTS4723-FOR (complementary to F13728) SEQ ID NO:13
 5' CUACUACUACUAGGAGTCCTCTACGGTGTTTTG and
 T42806-REV (complementary to T42806) SEQ ID NO:14
 5' CAUCAUCAUATGATGCTCAAGCTGAACTG. Five μ g of total RNA isolated from developing siliques of *Arabidopsis thaliana* was reverse transcribed using BRL Superscript RTase and the primer TSyn (5'-CCAAGCTTCTGCAGGAGCTCTTTTTTTTTTTTTTTT-3') and is shown as SEQ ID NO:12. PCR was carried out in a 50 μ l volume containing: template derived from 25 ng total RNA, 2 pM each primer, 200 μ M each deoxyribonucleotide triphosphate, 60 mM Tris-Cl, pH 8.5, 15 mM $(\text{NH}_4)_2\text{SO}_4$, 2 mM MgCl_2 , 0.2 U Taq Polymerase. Thermocycler conditions were as follows: 94 degrees for 30 sec., 50 degrees for 30 sec., 72 degrees for 30 sec. PCR was continued for 35 cycles followed by an additional extension at 72 degrees for 7 minutes. PCR resulted in a fragment of approximately ~750 base pairs which was subcloned, named 12-5, and sequenced. Each end of this fragment was formed to correspond to the *Arabidopsis* ESTs from which the PCR primers were designed. The putative amino acid sequence of 12-5 was compared to that of Ma524, and ESTs from human (W28140), mouse (W53753), and *C. elegans* (R05219) (see Figure 4). Homology patterns with the *Mortierella* $\Delta 6$ - desaturase indicate that these sequences represent putative

desaturase polypeptides. Based on this experiment approach, it is likely that the full-length genes can be cloned using probes based on the EST sequences.

Following the cloning, the genes can then be placed into expression vectors, expressed in host cells, and their specific $\Delta 6$ - or other desaturase activity can be determined as described below.

Example 4

Isolation of a $\Delta 12$ -desaturase Nucleotide Sequence from *Mortierella alpina*

Based on the fatty acids it accumulates, it seemed probable that *Mortierella alpina* has an $\omega 6$ type desaturase. The $\omega 6$ -desaturase is responsible for the production of linoleic acid (18:2) from oleic acid (18:1). Linoleic acid (18:2) is a substrate for a $\Delta 6$ -desaturase. This experiment was designed to determine if *Mortierella alpina* has a $\Delta 12$ -desaturase polypeptide, and if so, to identify the corresponding nucleotide sequence.

A random colony from the *M. alpina* sequencing grade library, Ma648, was sequenced and identified as a putative desaturase based on DNA sequence homology to previously identified desaturases, as described for Ma524 (*see* Example 2). The nucleotide sequence is shown in SEQ ID NO:13. The peptide sequence is shown in SEQ ID NO:4. The deduced amino acid sequence from the 5' end of the Ma648 cDNA displays significant homology to soybean microsomal $\omega 6$ ($\Delta 12$) desaturase (accession #L43921) as well as castor bean oleate 12-hydroxylase (accession #U22378). In addition, homology was observed when compared to a variety of other $\omega 6$ ($\Delta 12$) and $\omega 3$ ($\Delta 15$) fatty acid desaturase sequences.

Example 5

Expression of *M. alpina* Desaturase Clones in Baker's Yeast

Yeast Transformation

Lithium acetate transformation of yeast was performed according to standard protocols (*Methods in Enzymology*, Vol. 194, p. 186-187, 1991). Briefly, yeast were grown in YPD at 30°C. Cells were spun down, resuspended in TE, spun down again, resuspended in TE containing 100 mM lithium acetate, spun down again, and resuspended in TE/lithium acetate. The resuspended yeast were incubated at 30°C for 60 minutes with shaking. Carrier DNA was added, and the yeast were aliquoted into tubes. Transforming DNA was added, and the tubes were incubated for 30 min. at 30°C. PEG solution (35% (w/v) PEG 4000, 100 mM lithium acetate, TE pH7.5) was added followed by a 50 min. incubation at 30°C. A 5 min. heat shock at 42°C was performed, the cells were pelleted, washed with TE, pelleted again and resuspended in TE. The resuspended cells were then plated on selective media.

Desaturase Expression in Transformed Yeast

cDNA clones from *Mortierella alpina* were screened for desaturase activity in baker's yeast. A canola $\Delta 15$ -desaturase (obtained by PCR using 1st strand cDNA from *Brassica napus* cultivar 212/86 seeds using primers based on the published sequence (Arondel *et al. Science* 258:1353-1355)) was used as a positive control. The $\Delta 15$ -desaturase gene and the gene from cDNA clones Ma524 and Ma648 were put in the expression vector pYES2 (Invitrogen), resulting in plasmids pCGR-2, pCGR-5 and pCGR-7, respectively. These plasmids were transfected into *S. cerevisiae* yeast strain 334 and expressed after induction with galactose and in the presence of substrates that allowed detection of specific desaturase activity. The control strain was *S. cerevisiae* strain 334 containing the unaltered pYES2 vector. The substrates used, the products produced and the indicated desaturase activity were: DGLA (conversion to ARA would indicate $\Delta 5$ -desaturase activity), linoleic acid (conversion to GLA

would indicate $\Delta 6$ -desaturase activity; conversion to ALA would indicate $\Delta 15$ -desaturase activity), oleic acid (an endogenous substrate made by *S. cerevisiae*, conversion to linoleic acid would indicate $\Delta 12$ -desaturase activity, which *S. cerevisiae* lacks), or ARA (conversion to EPA would indicate $\Delta 17$ -desaturase activity).

Cultures were grown for 48-52 hours at 15°C in the presence of a particular substrate. Lipid fractions were extracted for analysis as follows: Cells were pelleted by centrifugation, washed once with sterile ddH₂O, and repelleted. Pellets were vortexed with methanol; chloroform was added along with tritridecanoin (as an internal standard). The mixtures were incubated for at least one hour at room temperature or at 4°C overnight. The chloroform layer was extracted and filtered through a Whatman filter with one gram of anhydrous sodium sulfate to remove particulates and residual water. The organic solvents were evaporated at 40°C under a stream of nitrogen. The extracted lipids were then derivatized to fatty acid methyl esters (FAME) for gas chromatography analysis (GC) by adding 2 ml of 0.5 N potassium hydroxide in methanol to a closed tube. The samples were heated to 95°C to 100°C for 30 minutes and cooled to room temperature. Approximately 2 ml of 14 % boron trifluoride in methanol was added and the heating repeated. After the extracted lipid mixture cooled, 2 ml of water and 1 ml of hexane were added to extract the FAME for analysis by GC. The percent conversion was calculated by dividing the product produced by the sum of (the product produced and the substrate added) and then multiplying by 100. To calculate the oleic acid percent conversion, as no substrate was added, the total linoleic acid produced was divided by the sum of oleic acid and linoleic acid produced, then multiplying by 100. The desaturase activity results are provided in Table 1 below.

Table 1***M. alpina* Desaturase Expression in Baker's Yeast**

CLONE	ENZYME ACTIVITY	% CONVERSION OF SUBSTRATE
pCGR-2	$\Delta 6$	0 (18:2 to 18:3w6)
(canola $\Delta 15$ desaturase)	$\Delta 15$	16.3 (18:2 to 18:3w3)
	$\Delta 5$	2.0 (20:3 to 20:4w6)
	$\Delta 17$	2.8 (20:4 to 20:5w3)
	$\Delta 12$	1.8 (18:1 to 18:2w6)
pCGR-5	$\Delta 6$	6.0
(M. alpina	$\Delta 15$	0
Ma524	$\Delta 5$	2.1
	$\Delta 17$	0
	$\Delta 12$	3.3
pCGR-7	$\Delta 6$	0
(M. alpina	$\Delta 15$	3.8
Ma648	$\Delta 5$	2.2
	$\Delta 17$	0
	$\Delta 12$	63.4

The $\Delta 15$ -desaturase control clone exhibited 16.3% conversion of the
 substrate. The pCGR-5 clone expressing the Ma524 cDNA showed 6%
 conversion of the substrate to GLA, indicating that the gene encodes a $\Delta 6$ -
 desaturase. The pCGR-7 clone expressing the Ma648 cDNA converted 63.4%
 conversion of the substrate to LA, indicating that the gene encodes a $\Delta 12$ -
 desaturase. The background (non-specific conversion of substrate) was between
 0-3% in these cases. We also found substrate inhibition of the activity by using
 different concentrations of the substrate. When substrate was added to 100 μ M,
 the percent conversion to product dropped compared to when substrate was added
 to 25 μ M (see below). Additionally, by varying the substrate concentration
 between 5 μ M and 200 μ M, conversion ratios were found to range between about

5% to about 75% greater. These data show that desaturases with different substrate specificities can be expressed in a heterologous system and used to produce poly-unsaturated long chain fatty acids.

Table 2 represents fatty acids of interest as a percent of the total lipid extracted from the yeast host *S. cerevisiae* 334 with the indicated plasmid. No glucose was present in the growth media. Affinity gas chromatography was used to separate the respective lipids. GC/MS was employed to verify the identity of the product(s). The expected product for the *B. napus* $\Delta 15$ -desaturase, α -linolenic acid, was detected when its substrate, linoleic acid, was added exogenously to the induced yeast culture. This finding demonstrates that yeast expression of a desaturase gene can produce functional enzyme and detectable amounts of product under the current growth conditions. Both exogenously added substrates were taken up by yeast, although slightly less of the longer chain PUFA, dihomo- γ -linolenic acid (20:3), was incorporated into yeast than linoleic acid (18:2) when either was added in free form to the induced yeast cultures. γ -linolenic acid was detected when linoleic acid was present during induction and expression of *S. cerevisiae* 334 (pCGR-5). The presence of this PUFA demonstrates $\Delta 6$ -desaturase activity from pCGR-5 (MA524). Linoleic acid, identified in the extracted lipids from expression of *S. cerevisiae* 334 (pCGR-7), classifies the cDNA MA648 from *M. alpina* as the $\Delta 12$ -desaturase.

Table 2
Fatty Acid as a Percentage of Total Lipid Extracted from Yeast

Plasmid in Yeast (enzyme)	18:2 Incorporated	α -18:3 Produced	γ -18:3 Produced	20:3 Incorporated	20:4 Produced	18:1* Present	18:2 Produced
pYES2 (control)	66.9	0	0	58.4	0	4	0
pCGR-2 (Δ 15)	60.1	5.7	0	50.4	0	0.7	0
pCGR-5 (Δ 6)	62.4	0	4.0	49.9	0	2.4	0
pCGR-7 (Δ 12)	65.6	0	0	45.7	0	7.1	12.2

100 μ M substrate added

* 18:1 is an endogenous fatty acid in yeast

Key To Tables

18:1=oleic acid
 18:2=linoleic acid
 α -18:3= α -linolenic acid
 γ -18:3= γ -linolenic acid
 18:4=stearidonic acid
 20:3=dihomo- γ -linolenic acid
 20:4=arachidonic acid

Example 6

Optimization of Culture Conditions

Table 3A shows the effect of exogenous free fatty acid substrate concentration on yeast uptake and conversion to fatty acid product as a percentage of the total yeast lipid extracted. In all instances, low amounts of exogenous substrate (1-10 μ M) resulted in low fatty acid substrate uptake and product formation. Between 25 and 50 μ M concentration of free fatty acid in the growth and induction media gave the highest percentage of fatty acid product formed, while the 100 μ M concentration and subsequent high uptake into yeast appeared to decrease or inhibit the desaturase activity. The amount of fatty acid substrate for yeast expressing Δ 12-desaturase was similar under the same growth conditions, since the substrate, oleic acid, is an endogenous yeast fatty acid. The use of α -linolenic acid as an additional substrate for pCGR-5 (Δ 6) produced the expected product, stearidonic acid (Table 3A). The feedback inhibition of high fatty acid substrate concentration was well illustrated when the percent conversion rates of the respective fatty acid substrates to their respective products were compared in Table 3B. In all cases, 100 μ M substrate concentration in the growth media decreased the percent conversion to product. The uptake of α -linolenic was comparable to other PUFAs added in free form, while the Δ 6-desaturase percent conversion, 3.8-17.5%, to the product stearidonic acid was the lowest of all the substrates examined (Table 3B). The effect of media, such as YPD (rich media) versus minimal media with glucose on the conversion rate of Δ 12-desaturase was dramatic. Not only did the conversion rate for oleic to linoleic acid drop, (Table 3B) but the percent of linoleic acid formed also decreased by 11% when rich media was used for growth and induction of yeast desaturase Δ 12 expression (Table 3A). The effect of media composition was also evident when glucose was present in the growth media for Δ 6-desaturase, since the percent of substrate uptake was decreased at 25 μ M (Table 3A). However, the conversion rate remained the

same and percent product formed decreased for $\Delta 6$ -desaturase for in the presence of glucose.

Table 3A

5

**Effect of Added Substrate on the Percentage of Incorporated
Substrate and Product Formed in Yeast Extracts**

Plasmid in Yeast	pCGR-2 ($\Delta 15$)	PcGR-5 ($\Delta 6$)	pCGR-5 ($\Delta 6$)	pCGR-7 ($\Delta 12$)
Substrate/product	18:2 / α -18:3	18:2/ γ -18:3	α -18:3/18:4	18:1*/18:2
1 μ M sub.	ND	0.9/0.7	ND	ND
10 μ M sub.	ND	4.2/2.4	10.4/2.2	ND
25 μ M sub.	ND	11/3.7	18.2/2.7	ND
25 μ M ϕ sub.	36.6/7.2 ϕ	25.1/10.3 ϕ	ND	6.6/15.8 ϕ
50 μ M sub.	53.1/6.5 ϕ	ND	36.2/3	10.8/13 ⁺
100 μ M sub.	60.1/5.7 ϕ	62.4/4 ϕ	47.7/1.9	10/24.8

Table 3B

**Effect of Substrate Concentration in Media on the Percent Conversion
of Fatty Acid Substrate to Product in Yeast Extracts**

Plasmid in Yeast	pCGR-2 ($\Delta 15$)	pCGR-5 ($\Delta 6$)	pCGR-5 ($\Delta 6$)	pCGR-7 ($\Delta 12$)
substrate→product	18:2 → α -18:3	18:2→ γ 18:3	α -18:3→18:4	18:1*→18:2
1 μ M sub.	ND	43.8	ND	ND
10 μ M sub.	ND	36.4	17.5	ND
25 μ M sub.	ND	25.2	12.9	ND
25 μ M \diamond sub.	16.4 \diamond	29.1 \diamond	ND	70.5 \diamond
50 μ M sub.	10.9 \diamond	ND	7.7	54.6 ⁺
100 μ M sub.	8.7 \diamond	6 \diamond	3.8	71.3

\diamond no glucose in media

⁺ Yeast peptone broth (YPD)

* 18:1 is an endogenous yeast lipid

sub. is substrate concentration

ND (not done)

Table 4 shows the amount of fatty acid produced by a recombinant desaturase from induced yeast cultures when different amounts of free fatty acid substrate were used. Fatty acid weight was determined since the total amount of lipid varied dramatically when the growth conditions were changed, such as the presence of glucose in the yeast growth and induction media. To better determine the conditions when the recombinant desaturase would produce the most PUFA product, the quantity of individual fatty acids were examined. The absence of glucose dramatically reduced by three fold the amount of linoleic acid produced by recombinant $\Delta 12$ -desaturase. For the $\Delta 12$ -desaturase the amount of total yeast lipid was decreased by almost half in the absence of glucose. Conversely, the presence of glucose in the yeast growth media for $\Delta 6$ -desaturase drops the γ -linolenic acid produced by almost half, while the total amount of yeast lipid produced was not changed by the presence/absence of

glucose. This points to a possible role for glucose as a modulator of $\Delta 6$ -desaturase activity.

Table 4

Fatty Acid Produced in μg from Yeast Extracts

Plasmid in Yeast (enzyme)	pCGR-5 ($\Delta 6$)	pCGR-5 ($\Delta 6$)	pCGR-7 ($\Delta 12$)
product	γ -18:3	18:4	18:2*
1 μM sub.	1.9	ND	ND
10 μM sub.	5.3	4.4	ND
25 μM sub.	10.3	8.7	115.7
25 μM \diamond sub.	29.6	ND	39 \diamond

\diamond no glucose in media

sub. is substrate concentration

ND (not done)

*18:1, the substrate, is an endogenous yeast lipid

Example 7

Distribution of PUFAs in Yeast Lipid Fractions

Table 5 illustrates the uptake of free fatty acids and their new products formed in yeast lipids as distributed in the major lipid fractions. A total lipid extract was prepared as described above. The lipid extract was separated on TLC plates, and the fractions were identified by comparison to standards. The bands were collected by scraping, and internal standards were added. The fractions were then saponified and methylated as above, and subjected to gas chromatography. The gas chromatograph calculated the amount of fatty acid by comparison to a standard. The phospholipid fraction contained the highest amount of substrate and product PUFAs for $\Delta 6$ -desaturase activity. It would appear that the substrates are accessible in the phospholipid form to the desaturases.

Table 5

Fatty Acid Distribution in Various Yeast Lipid Fractions in μg

Fatty acid fraction	Phospholipid	Diglyceride	Free Fatty Acid	Triglyceride	Cholesterol Ester
SC (pCGR-5) substrate 18:2	166.6	6.2	15	18.2	15.6
SC (pCGR-5) product γ -18:3	61.7	1.6	4.2	5.9	1.2

SC = *S. cerevisiae* (plasmid)Example 8Further Culture Optimization and Coexpression of $\Delta 6$ and $\Delta 12$ -desaturases

This experiment was designed to evaluate the growth and induction conditions for optimal activities of desaturases in *Saccharomyces cerevisiae*. A *Saccharomyces cerevisiae* strain (SC334) capable of producing γ -linolenic acid (GLA) was developed, to assess the feasibility of production of PUFA in yeast. The genes for $\Delta 6$ and $\Delta 12$ -desaturases from *M. alpina* were coexpressed in SC334. Expression of $\Delta 12$ -desaturase converted oleic acid (present in yeast) to linoleic acid. The linoleic acid was used as a substrate by the $\Delta 6$ -desaturase to produce GLA. The quantity of GLA produced ranged between 5-8% of the total fatty acids produced in SC334 cultures and the conversion rate of linoleic acid to γ -linolenic acid ranged between 30% to 50%. The induction temperature was optimized, and the effect of changing host strain and upstream promoter sequences on expression of $\Delta 6$ and $\Delta 12$ (MA 524 and MA 648 respectively) desaturase genes was also determined.

Plasmid Construction

The cloning of pCGR5 as well as pCGR7 has been discussed above. To construct pCGR9a and pCGR9b, the $\Delta 6$ and $\Delta 12$ -desaturase genes were amplified using the following sets of primers. The primers pRDS1 and 3 had XhoI site and primers pRDS2 and 4 had XbaI site (indicated in bold). These primer sequences are presented as SEQ ID NO:15-18.

I. $\Delta 6$ -desaturase amplification primers

a. pRDS1 TAC CAA **CTC GAG** AAA ATG GCT GCT GCT CCC
AGT GTG AGG

b. pRDS2 AAC TGA **TCT AGA** TTA CTG CGC CTT ACC CAT
CTT GGA GGC

II. $\Delta 12$ -desaturase amplification primers

a. pRDS3 TAC CAA **CTC GAG** AAA ATG GCA CCT CCC
AAC ACT ATC GAT

b. pRDS4 AAC TGA **TCT AGA** TTA CTT CTT GAA AAA GAC
CAC GTC TCC

The pCGR5 and pCGR7 constructs were used as template DNA for amplification of $\Delta 6$ and $\Delta 12$ -desaturase genes, respectively. The amplified products were digested with XbaI and XhoI to create "sticky ends". The PCR amplified $\Delta 6$ -desaturase with XhoI-XbaI ends as cloned into pCGR7, which was also cut with XhoI-XbaI. This procedure placed the $\Delta 6$ -desaturase behind the $\Delta 12$ -desaturase, under the control of an inducible promoter GAL1. This construct was designated pCGR9a. Similarly, to construct pCGR9b, the $\Delta 12$ -desaturase with XhoI-XbaI ends was cloned in the XhoI-XbaI sites of pCGR5. In pCGR9b the $\Delta 12$ -desaturase was behind the $\Delta 6$ -desaturase gene, away from the GAL promoter.

To construct pCGR10, the vector pRS425, which contains the constitutive Glyceraldehyde 3-Phosphate Dehydrogenase (GPD) promoter, was digested with BamHI and pCGR5 was digested with BamHI-XhoI to release the

$\Delta 6$ -desaturase gene. This $\Delta 6$ -desaturase fragment and BamHI cut pRS425 were filled using Klenow Polymerase to create blunt ends and ligated, resulting in pCGR10a and pCGR10b containing the $\Delta 6$ -desaturase gene in the sense and antisense orientation, respectively. To construct pCGR11 and pCGR12, the $\Delta 6$ and $\Delta 12$ -desaturase genes were isolated from pCGR5 and pCGR7, respectively, using an EcoRI-XhoI double digest. The EcoRI-XhoI fragments of $\Delta 6$ and $\Delta 12$ -desaturases were cloned into the pYX242 vector digested with EcoRI-XhoI. The pYX242 vector has the promoter of TPI (a yeast housekeeping gene), which allows constitutive expression.

10 **Yeast Transformation and Expression**

Different combinations of pCGR5, pCGR7, pCGR9a, pCGR9b, pCGR10a, pCGR11 and pCGR12 were introduced into various host strains of *Saccharomyces cerevisiae*. Transformation was done using PEG/LiAc protocol (Methods in Enzymology Vol. 194 (1991): 186-187). Transformants were selected by plating on synthetic media lacking the appropriate amino acid. The pCGR5, pCGR7, pCGR9a and pCGR9b can be selected on media lacking uracil. The pCGR10, pCGR11 and pCGR12 constructs can be selected on media lacking leucine. Growth of cultures and fatty acid analysis was performed as in Example 5 above.

20 **Production of GLA**

Production of GLA requires the expression of two enzymes (the $\Delta 6$ and $\Delta 12$ -desaturases), which are absent in yeast. To express these enzymes at optimum levels the following constructs or combinations of constructs, were introduced into various host strains:

- 25
- 1) pCGR9a/SC334
 - 2) pCGR9b/SC334
 - 3) pCGR10a and pCGR7/SC334
 - 4) pCGR11 and pCGR7/SC334
 - 5) pCGR12 and pCGR5/SC334

6) pCGR10a and pCGR7/DBY746

7) pCGR10a and pCGR7/DBY746

The pCGR9a construct has both the $\Delta 6$ and $\Delta 12$ -desaturase genes under the control of an inducible GAL promoter. The SC334 host cells transformed with this construct did not show any GLA accumulation in total fatty acids (Fig. 6A and B, lane 1). However, when the $\Delta 6$ and $\Delta 12$ -desaturase genes were individually controlled by the GAL promoter, the control constructs were able to express $\Delta 6$ - and $\Delta 12$ -desaturase, as evidenced by the conversion of their respective substrates to products. The $\Delta 12$ -desaturase gene in pCGR9a was expressed as evidenced by the conversion of 18:1 ω 9 to 18:2 ω 6 in pCGR9a/SC334, while the $\Delta 6$ -desaturase gene was not expressed/active, because the 18:2 ω 6 was not being converted to 18:3 ω 6 (Fig. 6A and B, lane 1).

The pCGR9b construct also had both the $\Delta 6$ and $\Delta 12$ -desaturase genes under the control of the GAL promoter but in an inverse order compared to pCGR9a. In this case, very little GLA (<1%) was seen in pCGR9b/SC334 cultures. The expression of $\Delta 12$ -desaturase was also very low, as evidenced by the low percentage of 18:2 ω 6 in the total fatty acids (Fig. 6A and B, lane 1).

To test if expressing both enzymes under the control of independent promoters would increase GLA production, the $\Delta 6$ -desaturase gene was cloned into the pRS425 vector. The construct of pCGR10a has the $\Delta 6$ -desaturase in the correct orientation, under control of constitutive GPD promoter. The pCGR10b has the $\Delta 6$ -desaturase gene in the inverse orientation, and serves as the negative control. The pCGR10a/SC334 cells produced significantly higher levels of GLA (5% of the total fatty acids, Fig. 6, lane 3), compared to pCGR9a. Both the $\Delta 6$ and $\Delta 12$ -desaturase genes were expressed at high level because the conversion of 18:1 ω 9 \rightarrow 18:2 ω 6 was 65%, while the conversion of 18:2 ω 6 \rightarrow 18:3 ω 6 ($\Delta 6$ -desaturase) was 30% (Fig. 6, lane 3). As expected, the negative control pCGR10b/SC334 did not show any GLA.

To further optimize GLA production, the $\Delta 6$ and $\Delta 12$ genes were introduced into the pYX242 vector, creating pCGR11 and pCGR12

respectively. The pYX242 vector allows for constitutive expression by the TP1 promoter (Alber, T. and Kawasaki, G. (1982). *J. Mol. & Appl. Genetics* 1: 419). The introduction of pCGR11 and pCGR7 in SC334 resulted in approximately 8% of GLA in total fatty acids of SC334. The rate of conversion of 18:1 ω 9 \rightarrow 18:2 ω 6 and 18:2 ω 6 \rightarrow 18:3 ω 6 was approximately 50% and 44% respectively (Fig. 6A and B, lane 4). The presence of pCGR12 and pCGR5 in SC334 resulted in 6.6% GLA in total fatty acids with a conversion rate of approximately 50% for both 18:1 ω 9 to 18:2 ω 6 and 18:2 ω 6 to 18:3 ω 6, respectively (Fig. 6A and B, lane 5). Thus although the quantity of GLA in total fatty acids was higher in the pCGR11/pCGR7 combination of constructs, the conversion rates of substrate to product were better for the pCGR12/pCGR5 combination.

To determine if changing host strain would increase GLA production, pCGR10a and pCGR7 were introduced into the host strain BJ1995 and DBY746 (obtained from the Yeast Genetic Stock Centre, 1021 Donner Laboratory, Berkeley, CA 94720. The genotype of strain DBY746 is Mat α , his3- Δ 1, leu2-3, leu2-112, ura3-32, trp1-289, gal). The results are shown in Fig. 7. Changing host strain to BJ1995 did not improve the GLA production, because the quantity of GLA was only 1.31% of total fatty acids and the conversion rate of 18:1 ω 9 \rightarrow 18:2 ω 6 was approximately 17% in BJ1995. No GLA was observed in DBY746 and the conversion of 18:1 ω 9 \rightarrow 18:2 ω 6 was very low (<1% in control) suggesting that a cofactor required for the expression of Δ 12-desaturase might be missing in DB746 (Fig. 7, lane 2).

To determine the effect of temperature on GLA production, SC334 cultures containing pCGR10a and pCGR7 were grown at 15°C and 30°C. Higher levels of GLA were found in cultures grown and induced at 15°C than those in cultures grown at 30°C (4.23% vs. 1.68%). This was due to a lower conversion rate of 18:2 ω 6 \rightarrow 18:3 ω 6 at 30°C (11.6% vs. 29% in 15°C) cultures, despite a higher conversion of 18:1 ω 9 \rightarrow 18:2 ω 6 (65% vs. 60% at 30°C (Fig. 8). These results suggest that Δ 12- and Δ 6-desaturases may have different optimal expression temperatures.

Of the various parameters examined in this study, temperature of growth, yeast host strain and media components had the most significant impact on the expression of desaturase, while timing of substrate addition and concentration of inducer did not significantly affect desaturase expression.

5 These data show that two DNAs encoding desaturases that can convert LA to GLA or oleic acid to LA can be isolated from *Mortierella alpina* and can be expressed, either individually or in combination, in a heterologous system and used to produce poly-unsaturated long chain fatty acids. Exemplified is the production of GLA from oleic acid by expression of $\Delta 12$ - and $\Delta 6$ -desaturases in
10 yeast.

Example 9

Identification of Homologues to *M. alpina* $\Delta 5$ and $\Delta 6$ desaturases

15 A nucleic acid sequence that encodes a putative $\Delta 5$ desaturase was identified through a TBLASTN search of the expressed sequence tag databases through NCBI using amino acids 100-446 of Ma29 as a query. The truncated portion of the Ma29 sequence was used to avoid picking up homologies based on the cytochrome b5 portion at the N-terminus of the desaturase. The deduced amino acid sequence of an est from *Dictyostelium discoideum* (accession # C25549) shows very significant homology to Ma29 and lesser, but still
20 significant homology to Ma524. The DNA sequence is presented as SEQ ID NO:19. The amino acid sequence is presented as SEQ ID NO:20.

Example 10

Identification of *M. alpina* $\Delta 5$ and $\Delta 6$ homologues in other PUFA-producing organisms

25 To look for desaturases involved in PUFA production, a cDNA library was constructed from total RNA isolated from *Phaeodactylum tricornutum*. A plasmid-based cDNA library was constructed in pSPORT1 (GIBCO-BRL)

following manufacturer's instructions using a commercially available kit (GIBCO-BRL). Random cDNA clones were sequenced and nucleic acid sequences that encode putative $\Delta 5$ or $\Delta 6$ desaturases were identified through BLAST search of the databases and comparison to Ma29 and Ma524 sequences.

- 5 One clone was identified from the *Phaeodactylum* library with homology to Ma29 and Ma524; it is called 144-011-B12. The DNA sequence is presented as SEQ ID NO:21. The amino acid sequence is presented as SEQ ID NO:22.

Example 11

10 **Identification of *M. alpina* $\Delta 5$ and $\Delta 6$ homologues in other PUFA-producing organisms**

- To look for desaturases involved in PUFA production, a cDNA library was constructed from total RNA isolated from *Schizochytrium* species. A plasmid-based cDNA library was constructed in pSPORT1 (GIBCO-BRL) following manufacturer's instructions using a commercially available kit (GIBCO-BRL). Random cDNA clones were sequenced and nucleic acid sequences that encode putative $\Delta 5$ or $\Delta 6$ desaturases were identified through BLAST search of the databases and comparison to Ma29 and Ma524 sequences.

- One clone was identified from the *Schizochytrium* library with homology to Ma29 and Ma524; it is called 81-23-C7. This clone contains a ~1 kb insert. Partial sequence was obtained from each end of the clone using the universal forward and reverse sequencing primers. The DNA sequence from the forward primer is presented as SEQ ID NO:23. The peptide sequence is presented as SEQ ID NO:24. The DNA sequence from the reverse primer is presented as SEQ ID NO:25. The amino acid sequence from the reverse primer is presented as SEQ ID NO:26.

Example 12

Human Desaturase Gene Sequences

Human desaturase gene sequences potentially involved in long chain polyunsaturated fatty acid biosynthesis were isolated based on homology between the human cDNA sequences and *Mortierella alpina* desaturase gene sequences. The three conserved "histidine boxes" known to be conserved among membrane-bound desaturases were found. As with some other membrane-bound desaturases the final HXXHH histidine box motif was found to be QXXHH. The amino acid sequence of the putative human desaturases exhibited homology to *M. alpina* $\Delta 5$, $\Delta 6$, $\Delta 9$, and $\Delta 12$ desaturases.

The *M. alpina* $\Delta 5$ desaturase and $\Delta 6$ desaturase cDNA sequences were used to search the LifeSeq database of Incyte Pharmaceuticals, Inc., Palo Alto, California 94304. The $\Delta 5$ desaturase sequence was divided into fragments; 1) amino acid no. 1-150, 2) amino acid no. 151-300, and 3) amino acid no. 301-446. The $\Delta 6$ desaturase sequence was divided into three fragments; 1) amino acid no. 1-150, 2) amino acid no. 151-300, and 3) amino acid no. 301-457. These polypeptide fragments were searched against the database using the "tblastn" algorithm. This algorithm compares a protein query sequence against a nucleotide sequence database dynamically translated in all six reading frames (both strands).

The polypeptide fragments 2 and 3 of *M. alpina* $\Delta 5$ and $\Delta 6$ have homologies with the CloneID sequences as outlined in Table 6. The CloneID represents an individual sequence from the Incyte LifeSeq database. After the "tblastn" results have been reviewed, Clone Information was searched with the default settings of Stringency of ≥ 50 , and Productscore ≤ 100 for different CloneID numbers. The Clone Information Results displayed the information including the ClusterID, CloneID, Library, HitID, Hit Description. When selected, the ClusterID number displayed the clone information of all the clones that belong in that ClusterID. The Assemble command assembles all of the CloneID which comprise the ClusterID. The following default settings were

used for GCG (Genetics Computer Group, University of Wisconsin Biotechnology Center, Madison, Wisconsin 53705) Assembly:

	Word Size:	7
5	Minimum Overlap:	14
	Stringency:	0.8
	Minimum Identity:	14
	Maximum Gap:	10
	Gap Weight:	8
10	Length Weight:	2

GCG Assembly Results displayed the contigs generated on the basis of sequence information within the CloneID. A contig is an alignment of DNA sequences based on areas of homology among these sequences. A new sequence (consensus sequence) was generated based on the aligned DNA sequences within a contig. The contig containing the CloneID was identified, and the ambiguous sites of the consensus sequence was edited based on the alignment of the CloneIDs (see SEQ ID NO:27 - SEQ ID NO:32) to generate the best possible sequence. The procedure was repeated for all six CloneID listed in Table 6. This produced five unique contigs. The edited consensus sequences of the 5 contigs were imported into the Sequencher software program (Gene Codes Corporation, Ann Arbor, Michigan 48105). These consensus sequences were assembled. The contig 2511785 overlaps with contig 3506132, and this new contig was called 2535 (SEQ ID NO:33). The contigs from the Sequencher program were copied into the Sequence Analysis software package of GCG.

Each contig was translated in all six reading frames into protein sequences. The *M. alpina* $\Delta 5$ (MA29) and $\Delta 6$ (MA524) sequences were compared with each of the translated contigs using the FastA search (a Pearson

and Lipman search for similarity between a query sequence and a group of sequences of the same type (nucleic acid or protein)). Homology among these sequences suggest the open reading frames of each contig. The homology among the *M. alpina* $\Delta 5$ and $\Delta 6$ to contigs 2535 and 3854933 were utilized to create the final contig called 253538a. Figure 13 is the FastA match of the final contig 253538a and MA29, and Figure 14 is the FastA match of the final contig 253538a and MA524. The DNA sequences for the various contigs are presented in SEQ ID NO:27 -SEQ ID NO:33 The various peptide sequences are shown in SEQ ID NO:34 - SEQ ID NO: 40.

Although the open reading frame was generated by merging the two contigs, the contig 2535 shows that there is a unique sequence in the beginning of this contig which does not match with the contig 3854933. Therefore, it is possible that these contigs were generated from independent desaturase like human genes.

The contig 253538a contains an open reading frame encoding 432 amino acids. It starts with Gln (CAG) and ends with the stop codon (TGA). The contig 253538a aligns with both *M. alpina* $\Delta 5$ and $\Delta 6$ sequences, suggesting that it could be either of the desaturases, as well as other known desaturases which share homology with each other. The individual contigs listed in Table 18, as well as the intermediate contig 2535 and the final contig 253538a can be utilized to isolate the complete genes for human desaturases.

Uses of the human desaturases

These human sequences can be express in yeast and plants utilizing the procedures described in the preceding examples. For expression in mammalian cells transgenic animals, these genes may provide superior codon bias.

In addition, these sequences can be used to isolate related desaturase genes from other organisms.

Table 6

Sections of the Desaturases	Clone ID from LifeSeq Database	Keyword
-----------------------------	--------------------------------	---------

151-300 $\Delta 5$	3808675	fatty acid desaturase
301-446 $\Delta 5$	354535	$\Delta 6$
151-300 $\Delta 6$	3448789	$\Delta 6$
151-300 $\Delta 6$	1362863	$\Delta 6$
151-300 $\Delta 6$	2394760	$\Delta 6$
301-457 $\Delta 6$	3350263	$\Delta 6$

Example 13

I. INFANT FORMULATIONS

A. Isomil® Soy Formula with Iron.

5 Usage: As a beverage for infants, children and adults with an allergy or sensitivity to cow's milk. A feeding for patients with disorders for which lactose should be avoided: lactase deficiency, lactose intolerance and galactosemia.

Features:

- 10 • Soy protein isolate to avoid symptoms of cow's-milk-protein allergy or sensitivity
- Lactose-free formulation to avoid lactose-associated diarrhea
- Low osmolality (240 mOsm/kg water) to reduce risk of osmotic diarrhea.
- 15 • Dual carbohydrates (corn syrup and sucrose) designed to enhance carbohydrate absorption and reduce the risk of exceeding the absorptive capacity of the damaged gut.
- 1.8 mg of Iron (as ferrous sulfate) per 100 Calories to help prevent iron deficiency.
- 20 • Recommended levels of vitamins and minerals.
- Vegetable oils to provide recommended levels of essential fatty acids.
- Milk-white color, milk-like consistency and pleasant aroma.

Ingredients: (Pareve, ©) 85% water, 4.9% corn syrup, 2.6% sugar (sucrose), 2.1% soy oil, 1.9% soy protein isolate, 1.4% coconut oil, 0.15% calcium citrate, 0.11 % calcium phosphate tribasic, potassium citrate, potassium phosphate monobasic, potassium chloride, mono- and diglycerides, soy lecithin, carrageenan, ascorbic acid, L-methionine, magnesium chloride, potassium phosphate dibasic, sodium chloride, choline chloride, taurine, ferrous sulfate, m-inositol, alpha-tocopheryl acetate, zinc sulfate, L-carnitine, niacinamide, calcium pantothenate, cupric sulfate, vitamin A palmitate, thiamine chloride hydrochloride, riboflavin, pyridoxine hydrochloride, folic acid, manganese sulfate, potassium iodide, phylloquinone, biotin, sodium selenite, vitamin D₃ and cyanocobalamin.

B. Isomil® DF Soy Formula For Diarrhea.

Usage: As a short-term feeding for the dietary management of diarrhea in infants and toddlers.

Features:

- First infant formula to contain added dietary fiber from soy fiber specifically for diarrhea management.
- Clinically shown to reduce the duration of loose, watery stools during mild to severe diarrhea in infants.
- Nutritionally complete to meet the nutritional needs of the infant.
- Soy protein isolate with added L-methionine meets or exceeds an infant's requirement for all essential amino acids.
- Lactose-free formulation to avoid lactose-associated diarrhea.
- Low osmolality (240 mOsm/kg water) to reduce the risk of osmotic diarrhea.
- Dual carbohydrates (corn syrup and sucrose) designed to enhance carbohydrate absorption and reduce the risk of exceeding the absorptive capacity of the damaged gut.

- Meets or exceeds the vitamin and mineral levels recommended by the Committee on Nutrition of the American Academy of Pediatrics and required by the Infant Formula Act.

5

- 1.8 mg of iron (as ferrous sulfate) per 100 Calories to help prevent iron deficiency.

- Vegetable oils to provide recommended levels of essential fatty acids.

10

Ingredients: (Pareve, ☉) 86% water, 4.8% corn syrup, 2.5% sugar (sucrose), 2.1% soy oil, 2.0% soy protein isolate, 1.4% coconut oil, 0.77% soy fiber, 0.12% calcium citrate, 0.11 % calcium phosphate tribasic, 0.10% potassium citrate, potassium chloride, potassium phosphate monobasic, mono- and diglycerides, soy lecithin, carrageenan, magnesium chloride, ascorbic acid, L-methionine, potassium phosphate dibasic, sodium chloride, choline chloride, taurine, ferrous sulfate, m-inositol, alpha-tocopheryl acetate, zinc sulfate, L-

15 carnitine, niacinamide, calcium pantothenate, cupric sulfate, vitamin A palmitate, thiamine chloride hydrochloride, riboflavin, pyridoxine hydrochloride, folic acid, manganese sulfate, potassium iodide, phylloquinone, biotin, sodium selenite, vitamin D₃ and cyanocobalamin.

C. Isomil® SF Sucrose-Free Soy Formula With Iron.

20

Usage: As a beverage for infants, children and adults with an allergy or sensitivity to cow's-milk protein or an intolerance to sucrose. A feeding for patients with disorders for which lactose and sucrose should be avoided.

Features:

25

- Soy protein isolate to avoid symptoms of cow's-milk-protein allergy or sensitivity.
- Lactose-free formulation to avoid lactose-associated diarrhea (carbohydrate source is Polycose® Glucose Polymers).
- Sucrose free for the patient who cannot tolerate sucrose.

- Low osmolality (180 mOsm/kg water) to reduce risk of osmotic diarrhea.
- 1.8 mg of iron (as ferrous sulfate) per 100 Calories to help prevent iron deficiency.
- 5 • Recommended levels of vitamins and minerals.
- Vegetable oils to provide recommended levels of essential fatty acids.
- Milk-white color, milk-like consistency and pleasant aroma.

Ingredients: (Pareve, ®) 75% water, 11.8% hydrolyzed cornstarch, 4.1%
 10 soy oil, 4.1% soy protein isolate, 2.8% coconut oil, 1.0% modified cornstarch,
 0.38% calcium phosphate tribasic, 0.17% potassium citrate, 0.13% potassium
 chloride, mono- and diglycerides, soy lecithin, magnesium chloride, ascorbic
 acid, L-methionine, calcium carbonate, sodium chloride, choline chloride,
 15 carrageenan, taurine, ferrous sulfate, m-inositol, alpha-tocopheryl acetate, zinc
 sulfate, L-carnitine, niacinamide, calcium pantothenate, cupric sulfate, vitamin
 A palmitate, thiamine chloride hydrochloride, riboflavin, pyridoxine
 hydrochloride, folic acid, manganese sulfate, potassium iodide, phylloquinone,
 biotin, sodium selenite, vitamin D₃ and cyanocobalamin.

**D. Isomil® 20 Soy Formula With Iron Ready To Feed,
 20 20 Cal/fl oz.**

Usage: When a soy feeding is desired.

Ingredients: (Pareve, ®) 85% water, 4.9% corn syrup, 2.6% sugar
 (sucrose), 2.1% soy oil, 1.9% soy protein isolate, 1.4% coconut oil, 0.15%
 calcium citrate, 0.11% calcium phosphate tribasic, potassium citrate, potassium
 25 phosphate monobasic, potassium chloride, mono- and diglycerides, soy
 lecithin, carrageenan, ascorbic acid, L-methionine, magnesium chloride,
 potassium phosphate dibasic, sodium chloride, choline chloride, taurine, ferrous
 sulfate, m-inositol, alpha-tocopheryl acetate, zinc sulfate, L-carnitine,
 niacinamide, calcium pantothenate, cupric sulfate, vitamin A palmitate,
 30 thiamine chloride hydrochloride, riboflavin, pyridoxine hydrochloride, folic

acid, manganese sulfate, potassium iodide, phylloquinone, biotin, sodium selenite, vitamin D₃ and cyanocobalamin.

E. Similac® Infant Formula

5 Usage: When an infant formula is needed: if the decision is made to discontinue breastfeeding before age 1 year, if a supplement to breastfeeding is needed or as a routine feeding if breastfeeding is not adopted.

Features:

- 10 • Protein of appropriate quality and quantity for good growth; heat-denatured, which reduces the risk of milk-associated enteric blood loss.
- Fat from a blend of vegetable oils (doubly homogenized), providing essential linoleic acid that is easily absorbed.
- Carbohydrate as lactose in proportion similar to that of human milk.
- 15 • Low renal solute load to minimize stress on developing organs.
- Powder, Concentrated Liquid and Ready To Feed forms.

Ingredients: (©-D) Water, nonfat milk, lactose, soy oil, coconut oil, mono- and diglycerides, soy lecithin, ascorbic acid, carrageenan, choline chloride, taurine, m-inositol, alpha-tocopheryl acetate, zinc sulfate, niacinamid, 20 ferrous sulfate, calcium pantothenate, cupric sulfate, vitamin A palmitate, thiamine chloride hydrochloride, riboflavin, pyridoxine hydrochloride, folic acid, manganese sulfate, phylloquinone, biotin, sodium selenite, vitamin D₃ and cyanocobalamin.

F. Similac® NeoCare Premature Infant Formula With Iron

25 Usage: For premature infants' special nutritional needs after hospital discharge. Similac NeoCare is a nutritionally complete formula developed to provide premature infants with extra calories, protein, vitamins and minerals needed to promote catch-up growth and support development.

Features:

- Reduces the need for caloric and vitamin supplementation. More calories (22 Cal/fl oz) than standard term formulas (20 Cal/fl oz).
- Highly absorbed fat blend, with medium-chain triglycerides (MCT oil) to help meet the special digestive needs of premature infants.
- Higher levels of protein, vitamins and minerals per 100 Calories to extend the nutritional support initiated in-hospital.
- More calcium and phosphorus for improved bone mineralization.

Ingredients: ©-D Corn syrup solids, nonfat milk, lactose, whey protein concentrate, soy oil, high-oleic safflower oil, fractionated coconut oil (medium-chain triglycerides), coconut oil, potassium citrate, calcium phosphate tribasic, calcium carbonate, ascorbic acid, magnesium chloride, potassium chloride, sodium chloride, taurine, ferrous sulfate, m-inositol, choline chloride, ascorbyl palmitate, L-carnitine, alpha-tocopheryl acetate, zinc sulfate, niacinamide, mixed tocopherols, sodium citrate, calcium pantothenate, cupric sulfate, thiamine chloride hydrochloride, vitamin A palmitate, beta carotene, riboflavin, pyridoxine hydrochloride, folic acid, manganese sulfate, phylloquinone, biotin, sodium selenite, vitamin D₃ and cyanocobalamin.

G. Similac Natural Care Low-Iron Human Milk Fortifier Ready To Use, 24 Cal/fl oz.

Usage: Designed to be mixed with human milk or to be fed alternatively with human milk to low-birth-weight infants.

Ingredients: ©-D Water, nonfat milk, hydrolyzed cornstarch, lactose, fractionated coconut oil (medium-chain triglycerides), whey protein concentrate, soy oil, coconut oil, calcium phosphate tribasic, potassium citrate, magnesium chloride, sodium citrate, ascorbic acid, calcium carbonate, mono- and diglycerides, soy lecithin, carrageenan, choline chloride, m-inositol, taurine, niacinamide, L-carnitine, alpha tocopheryl acetate, zinc sulfate, potassium chloride, calcium pantothenate, ferrous sulfate, cupric sulfate, riboflavin, vitamin A palmitate, thiamine chloride hydrochloride, pyridoxine

hydrochloride, biotin, folic acid, manganese sulfate, phylloquinone, vitamin D₃, sodium selenite and cyanocobalamin.

Various PUFAs of this invention can be substituted and/or added to the infant formulae described above and to other infant formulae known to those in the art..

II. NUTRITIONAL FORMULATIONS

A. ENSURE®

Usage: ENSURE is a low-residue liquid food designed primarily as an oral nutritional supplement to be used with or between meals or, in appropriate amounts, as a meal replacement. ENSURE is lactose- and gluten-free, and is suitable for use in modified diets, including low-cholesterol diets. Although it is primarily an oral supplement, it can be fed by tube.

Patient Conditions:

- For patients on modified diets
- For elderly patients at nutrition risk
- For patients with involuntary weight loss
- For patients recovering from illness or surgery
- For patients who need a low-residue diet

Ingredients:

• D Water, Sugar (Sucrose), Maltodextrin (Corn), Calcium and Sodium Caseinates, High-Oleic Safflower Oil, Soy Protein Isolate, Soy Oil, Canola Oil, Potassium Citrate, Calcium Phosphate Tribasic, Sodium Citrate, Magnesium Chloride, Magnesium Phosphate Dibasic, Artificial Flavor, Sodium Chloride, Soy Lecithin, Choline Chloride, Ascorbic Acid, Carrageenan, Zinc Sulfate, Ferrous Sulfate, Alpha-Tocopheryl Acetate, Gellan Gum, Niacinamide, Calcium Pantothenate, Manganese Sulfate, Cupric Sulfate, Vitamin A Palmitate, Thiamine Chloride Hydrochloride, Pyridoxine Hydrochloride, Riboflavin, Folic Acid, Sodium Molybdate, Chromium Chloride, Biotin, Potassium Iodide, Sodium Selenate.

B. ENSURE® BARS

Usage: ENSURE BARS are complete, balanced nutrition for supplemental use between or with meals. They provide a delicious, nutrient-rich alternative to other snacks. ENSURE BARS contain <1 g lactose/bar, and Chocolate Fudge Brownie flavor is gluten-free. (Honey Graham Crunch flavor contains gluten.)

Patient Conditions:

- For patients who need extra calories, protein, vitamins and minerals
- Especially useful for people who do not take in enough calories and nutrients
- For people who have the ability to chew and swallow
- Not to be used by anyone with a peanut allergy or any type of allergy to nuts.

Ingredients:

Honey Graham Crunch -- High-Fructose Corn Syrup, Soy Protein Isolate, Brown Sugar, Honey, Maltodextrin (Corn), Crisp Rice (Milled Rice, Sugar [Sucrose], Salt [Sodium Chloride] and Malt), Oat Bran, Partially Hydrogenated Cottonseed and Soy Oils, Soy Polysaccharide, Glycerine, Whey Protein Concentrate, Polydextrose, Fructose, Calcium Caseinate, Cocoa Powder, Artificial Flavors, Canola Oil, High-Oleic Safflower Oil, Nonfat Dry Milk, Whey Powder, Soy Lecithin and Corn Oil. Manufactured in a facility that processes nuts.

Vitamins and Minerals:

Calcium Phosphate Tribasic, Potassium Phosphate Dibasic, Magnesium Oxide, Salt (Sodium Chloride), Potassium Chloride, Ascorbic Acid, Ferric Orthophosphate, Alpha-Tocopheryl Acetate, Niacinamide, Zinc Oxide, Calcium Pantothenate, Copper Gluconate, Manganese Sulfate, Riboflavin, Beta-Carotene, Pyridoxine Hydrochloride, Thiamine Mononitrate, Folic Acid, Biotin,

Chromium Chloride, Potassium Iodide, Sodium Selenate, Sodium Molybdate, Phylloquinone, Vitamin D₃ and Cyanocobalamin.

Protein:

5 **Honey Graham Crunch** - The protein source is a blend of soy protein isolate and milk proteins.

Soy protein isolate	74%
Milk proteins	26%

Fat:

10 **Honey Graham Crunch** - The fat source is a blend of partially hydrogenated cottonseed and soybean, canola, high oleic safflower, and corn oils, and soy lecithin.

Partially hydrogenated cottonseed and soybean oil	76%
Canola oil	8%
High-oleic safflower oil	8%
15 Corn oil	4%
Soy lecithin	4%

Carbohydrate:

20 **Honey Graham Crunch** - The carbohydrate source is a combination of high-fructose corn syrup, brown sugar, maltodextrin, honey, crisp rice, glycerine, soy polysaccharide, and oat bran.

High-fructose corn syrup	24%
Brown sugar	21%
Maltodextrin	12%
Honey	11%
25 Crisp rice	9%
Glycerine	9%
Soy polysaccharide	7%
Oat bran	7%\

C. ENSURE® HIGH PROTEIN

Usage: ENSURE HIGH PROTEIN is a concentrated, high-protein liquid food designed for people who require additional calories, protein, vitamins, and minerals in their diets. It can be used as an oral nutritional supplement with or between meals or, in appropriate amounts, as a meal replacement. ENSURE HIGH PROTEIN is lactose- and gluten-free, and is suitable for use by people recovering from general surgery or hip fractures and by patients at risk for pressure ulcers.

Patient Conditions

- For patients who require additional calories, protein, vitamins, and minerals, such as patients recovering from general surgery or hip fractures, patients at risk for pressure ulcers, and patients on low-cholesterol diets

Features-

- Low in saturated fat
- Contains 6 g of total fat and < 5 mg of cholesterol per serving
- Rich, creamy taste
- Excellent source of protein, calcium, and other essential vitamins and minerals
- For low-cholesterol diets
- Lactose-free, easily digested

Ingredients:

Vanilla Supreme: -D Water, Sugar (Sucrose), Maltodextrin (Corn), Calcium and Sodium Caseinates, High-Oleic Safflower Oil, Soy Protein Isolate, Soy Oil, Canola Oil, Potassium Citrate, Calcium Phosphate Tribasic, Sodium Citrate, Magnesium Chloride, Magnesium Phosphate Dibasic, Artificial Flavor, Sodium Chloride, Soy Lecithin, Choline Chloride, Ascorbic Acid, Carrageenan, Zinc Sulfate, Ferrous Sulfate, Alpha-Tocopheryl Acetate, Gellan Gum, Niacinamide, Calcium Pantothenate, Manganese Sulfate, Cupric Sulfate, Vitamin A Palmitate, Thiamine Chloride Hydrochloride, Pyridoxine Hydrochloride,

Riboflavin, Folic Acid, Sodium Molybdate, Chromium Chloride, Biotin, Potassium Iodide, Sodium Selenate, Phylloquinone, Vitamin D₃ and Cyanocobalamin.

Protein:

- 5 The protein source is a blend of two high-biologic-value proteins: casein and soy.

Sodium and calcium caseinates	85%
Soy protein isolate	15%

Fat:

- 10 The fat source is a blend of three oils: high-oleic safflower, canola, and soy.

High-oleic safflower oil	40%
Canola oil	30%
Soy oil	30%

- 15 The level of fat in ENSURE HIGH PROTEIN meets American Heart Association (AHA) guidelines. The 6 grams of fat in ENSURE HIGH PROTEIN represent 24% of the total calories, with 2.6% of the fat being from saturated fatty acids and 7.9% from polyunsaturated fatty acids. These values are within the AHA guidelines of $\leq 30\%$ of total calories from fat, $< 10\%$ of the calories from saturated fatty acids, and $\leq 10\%$ of total calories from
- 20 polyunsaturated fatty acids.

Carbohydrate:

- 25 ENSURE HIGH PROTEIN contains a combination of maltodextrin and sucrose. The mild sweetness and flavor variety (vanilla supreme, chocolate royal, wild berry, and banana), plus VARI-FLAVORSO® Flavor Pacs in pecan, cherry, strawberry, lemon, and orange, help to prevent flavor fatigue and aid in patient compliance.

Vanilla and other nonchocolate flavors

Sucrose	60%
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Maltodextrin	40%
--------------	-----

Chocolate

Sucrose	70%
---------	-----

Maltodextrin	30%
--------------	-----

5

D. ENSURE® LIGHT

Usage: ENSURE LIGHT is a low-fat liquid food designed for use as an oral nutritional supplement with or between meals. ENSURE LIGHT is lactose- and gluten-free, and is suitable for use in modified diets, including low-cholesterol diets.

10

Patient Conditions:

- For normal-weight or overweight patients who need extra nutrition in a supplement that contains 50% less fat and 20% fewer calories than ENSURE
- For healthy adults who don't eat right and need extra nutrition

15

Features:

- Low in fat and saturated fat
- Contains 3 g of total fat per serving and < 5 mg cholesterol
- Rich, creamy taste
- Excellent source of calcium and other essential vitamins and minerals
- For low-cholesterol diets
- Lactose-free, easily digested

20

Ingredients:

French Vanilla: ®-D Water, Maltodextrin (Corn), Sugar (Sucrose), Calcium Caseinate, High-Oleic Safflower Oil, Canola Oil, Magnesium Chloride, Sodium Citrate, Potassium Citrate, Potassium Phosphate Dibasic, Magnesium Phosphate Dibasic, Natural and Artificial Flavor, Calcium Phosphate Tribasic, Cellulose Gel, Choline Chloride, Soy Lecithin, Carrageenan, Salt (Sodium Chloride),

25

- Ascorbic Acid, Cellulose Gum, Ferrous Sulfate, Alpha-Tocopheryl Acetate, Zinc Sulfate, Niacinamide, Manganese Sulfate, Calcium Pantothenate, Cupric Sulfate, Thiamine Chloride Hydrochloride, Vitamin A Palmitate, Pyridoxine Hydrochloride, Riboflavin, Chromium Chloride, Folic Acid, Sodium Molybdate, Biotin, Potassium Iodide, Sodium Selenate, Phylloquinone, Vitamin D₃ and Cyanocobalamin.

Protein:

The protein source is calcium caseinate.

Calcium caseinate	100%
-------------------	------

10 Fat

The fat source is a blend of two oils: high-oleic safflower and canola.

High-oleic safflower oil	70%
Canola oil	30%

- The level of fat in ENSURE LIGHT meets American Heart Association (AHA) guidelines. The 3 grams of fat in ENSURE LIGHT represent 13.5% of the total calories, with 1.4% of the fat being from saturated fatty acids and 2.6% from polyunsaturated fatty acids. These values are within the AHA guidelines of $\leq 30\%$ of total calories from fat, $< 10\%$ of the calories from saturated fatty acids, and $\leq 10\%$ of total calories from polyunsaturated fatty acids.

20 Carbohydrate

ENSURE LIGHT contains a combination of maltodextrin and sucrose.

- The chocolate flavor contains corn syrup as well. The mild sweetness and flavor variety (French vanilla, chocolate supreme, strawberry swirl), plus VARI-FLAVORS® Flavor Pacs in pecan, cherry, strawberry, lemon, and orange, help to prevent flavor fatigue and aid in patient compliance.

Vanilla and other nonchocolate flavors

Sucrose	51%
Maltodextrin	49%

Chocolate

Sucrose	47.0%
Corn Syrup	26.5%
Maltodextrin	26.5%

5 **Vitamins and Minerals**

An 8-fl-oz serving of ENSURE LIGHT provides at least 25% of the RDIs for 24 key vitamins and minerals.

Caffeine

Chocolate flavor contains 2.1 mg caffeine/8 fl oz.

10

E. ENSURE PLUS®

Usage: ENSURE PLUS is a high-calorie, low-residue liquid food for use when extra calories and nutrients, but a normal concentration of protein, are needed. It is designed primarily as an oral nutritional supplement to be used with or between meals or, in appropriate amounts, as a meal replacement. ENSURE PLUS is lactose- and gluten-free. Although it is primarily an oral nutritional supplement, it can be fed by tube.

15

Patient Conditions:

- For patients who require extra calories and nutrients, but a normal concentration of protein, in a limited volume
- For patients who need to gain or maintain healthy weight

20

Features

- Rich, creamy taste
- Good source of essential vitamins and minerals

25

Ingredients

Vanilla: ®-D Water, Corn Syrup, Maltodextrin (Corn), Corn Oil, Sodium and Calcium Caseinates, Sugar (Sucrose), Soy Protein Isolate, Magnesium Chloride,

Potassium Citrate, Calcium Phosphate Tribasic, Soy Lecithin, Natural and Artificial Flavor, Sodium Citrate, Potassium Chloride, Choline Chloride, Ascorbic Acid, Carrageenan, Zinc Sulfate, Ferrous Sulfate, Alpha-Tocopheryl Acetate, Niacinamide, Calcium Pantothenate, Manganese Sulfate, Cupric Sulfate, Thiamine Chloride Hydrochloride, Pyridoxine Hydrochloride, Riboflavin, Vitamin A Palmitate, Folic Acid, Biotin, Chromium Chloride, Sodium Molybdate, Potassium Iodide, Sodium Selenite, Phylloquinone, Cyanocobalamin and Vitamin D₃.

Protein

The protein source is a blend of two high-biologic-value proteins: casein and soy.

Sodium and calcium caseinates	84%
Soy protein isolate	16%

Fat

The fat source is corn oil.

Corn oil	100%
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Carbohydrate

ENSURE PLUS contains a combination of maltodextrin and sucrose. The mild sweetness and flavor variety (vanilla, chocolate, strawberry, coffee, butter pecan, and eggnog), plus VARI-FLAVORS® Flavor Pacs in pecan, cherry, strawberry, lemon, and orange, help to prevent flavor fatigue and aid in patient compliance.

Vanilla, strawberry, butter pecan, and coffee flavors

Corn Syrup	39%
Maltodextrin	38%
Sucrose	23%

Chocolate and eggnog flavors

Corn Syrup	36%
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Maltodextrin	34%
--------------	-----

Sucrose	30%
---------	-----

Vitamins and Minerals

5 An 8-fl-oz serving of ENSURE PLUS provides at least 15% of the RDIs for 25 key Vitamins and minerals.

Caffeine

Chocolate flavor contains 3.1 mg Caffeine/8 fl oz. Coffee flavor contains a trace amount of caffeine.

10 **F. ENSURE PLUS® HN**

Usage: ENSURE PLUS HN is a nutritionally complete high-calorie, high-nitrogen liquid food designed for people with higher calorie and protein needs or limited volume tolerance. It may be used for oral supplementation or for total nutritional support by tube. ENSURE PLUS HN is lactose- and gluten-free.

Patient Conditions:

- For patients with increased calorie and protein needs, such as following surgery or injury
- For patients with limited volume tolerance and early satiety

20 **Features**

- For supplemental or total nutrition
- For oral or tube feeding
- 1.5 CaVmL
- High nitrogen
- 25 • Calorically dense

Ingredients

Vanilla: ®-D Water, Maltodextrin (Corn), Sodium and Calcium Caseinates, Corn Oil, Sugar (Sucrose), Soy Protein Isolate, Magnesium Chloride, Potassium Citrate, Calcium Phosphate Tribasic, Soy Lecithin, Natural and Artificial Flavor, Sodium Citrate, Choline Chloride, Ascorbic Acid, Taurine, L-Carnitine, 5 Zinc Sulfate, Ferrous Sulfate, Alpha-Tocopheryl Acetate, Niacinamide, Carrageenan, Calcium Pantothenate, Manganese Sulfate, Cupric Sulfate, Thiamine Chloride Hydrochloride, Pyridoxine Hydrochloride, Riboflavin, Vitamin A Palmitate, Folic Acid, Biotin, Chromium Chloride, Sodium Molybdate, Potassium Iodide, Sodium Selenite, Phylloquinone, 10 Cyanocobalamin and Vitamin D₃.

G. ENSURE® POWDER

Usage: ENSURE POWDER (reconstituted with water) is a low-residue liquid food designed primarily as an oral nutritional supplement to be used with 15 or between meals. ENSURE POWDER is lactose- and gluten-free, and is suitable for use in modified diets, including low-cholesterol diets.

Patient Conditions:

- For patients on modified diets
- For elderly patients at nutrition risk
- 20 • For patients recovering from illness/surgery
- For patients who need a low-residue diet

Features

- Convenient, easy to mix
- Low in saturated fat
- 25 • Contains 9 g of total fat and < 5 mg of cholesterol per serving
- High in vitamins and minerals
- For low-cholesterol diets
- Lactose-free, easily digested

Ingredients: ®-D Corn Syrup, Maltodextrin (Corn), Sugar (Sucrose), Corn Oil, Sodium and Calcium Caseinates, Soy Protein Isolate, Artificial Flavor, Potassium Citrate, Magnesium Chloride, Sodium Citrate, Calcium Phosphate Tribasic, Potassium Chloride, Soy Lecithin, Ascorbic Acid, Choline Chloride, Zinc Sulfate, Ferrous Sulfate, Alpha-Tocopheryl Acetate, Niacinamide, Calcium Pantothenate, Manganese Sulfate, Thiamine Chloride Hydrochloride, Cupric Sulfate, Pyridoxine Hydrochloride, Riboflavin, Vitamin A Palmitate, Folic Acid, Biotin, Sodium Molybdate, Chromium Chloride, Potassium Iodide, Sodium Selenate, Phylloquinone, Vitamin D₃ and Cyanocobalamin.

10 **Protein**

The protein source is a blend of two high-biologic-value proteins: casein and soy.

Sodium and calcium caseinates	84%
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Soy protein isolate	16%
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15 **Fat**

The fat source is corn oil.

Corn oil	100%
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Carbohydrate

ENSURE POWDER contains a combination of corn syrup, maltodextrin, and sucrose. The mild sweetness of ENSURE POWDER, plus VARI-FLAVORS® Flavor Pacs in pecan, cherry, strawberry, lemon, and orange, helps to prevent flavor fatigue and aid in patient compliance.

Vanilla

Corn Syrup	35%
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Maltodextrin	35%
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Sucrose	30%
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H. ENSURE® PUDDING

Usage: ENSURE PUDDING is a nutrient-dense supplement providing balanced nutrition in a nonliquid form to be used with or between meals. It is appropriate for consistency-modified diets (e.g., soft, pureed, or full liquid) or for people with swallowing impairments. ENSURE PUDDING is gluten-free.

Patient Conditions:

- For patients on consistency-modified diets (e.g., soft, pureed, or full liquid)
- For patients with swallowing impairments

Features

- Rich and creamy, good taste
- Good source of essential vitamins and minerals Convenient-needs no refrigeration
- Gluten-free

Nutrient Profile per 5 oz: Calories 250, Protein 10.9%, Total Fat 34.9%, Carbohydrate 54.2%

Ingredients:

Vanilla: ®-D Nonfat Milk, Water, Sugar (Sucrose), Partially Hydrogenated Soybean Oil, Modified Food Starch, Magnesium Sulfate. Sodium Stearoyl Lactylate, Sodium Phosphate Dibasic, Artificial Flavor, Ascorbic Acid, Zinc Sulfate, Ferrous Sulfate, Alpha-Tocopheryl Acetate, Choline Chloride, Niacinamide, Manganese Sulfate, Calcium Pantothenate, FD&C Yellow #5, Potassium Citrate, Cupric Sulfate, Vitamin A Palmitate, Thiamine Chloride Hydrochloride, Pyridoxine Hydrochloride, Riboflavin, FD&C Yellow #6, Folic Acid, Biotin, Phylloquinone, Vitamin D3 and Cyanocobalamin.

Protein

The protein source is nonfat milk.

Nonfat milk

100%

Fat

The fat source is hydrogenated soybean oil.

Hydrogenated soybean oil	100%
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Carbohydrate

5 ENSURE PUDDING contains a combination of sucrose and modified food starch. The mild sweetness and flavor variety (vanilla, chocolate, butterscotch, and tapioca) help prevent flavor fatigue. The product contains 9.2 grams of lactose per serving.

Vanilla and other nonchocolate flavors

10	Sucrose	56%
	Lactose	27%
	Modified food starch	17%

Chocolate

	Sucrose	58%
15	Lactose	26%
	Modified food starch	16%

I. ENSURE® WITH FIBER

20 Usage: ENSURE WITH FIBER is a fiber-containing, nutritionally complete liquid food designed for people who can benefit from increased dietary fiber and nutrients. ENSURE WITH FIBER is suitable for people who do not require a low-residue diet. It can be fed orally or by tube, and can be used as a nutritional supplement to a regular diet or, in appropriate amounts, as a meal replacement. ENSURE WITH FIBER is lactose- and gluten-free, and is

25 suitable for use in modified diets, including low-cholesterol diets.

Patient Conditions

- For patients who can benefit from increased dietary fiber and nutrients

Features

- New advanced formula-low in saturated fat, higher in vitamins and minerals
- Contains 6 g of total fat and < 5 mg of cholesterol per serving
- Rich, creamy taste
- 5 • Good source of fiber
- Excellent source of essential vitamins and minerals
- For low-cholesterol diets
- Lactose- and gluten-free

Ingredients

- 10 **Vanilla:** ®-D Water, Maltodextrin (Corn), Sugar (Sucrose), Sodium and Calcium Caseinates, Oat Fiber, High-Oleic Safflower Oil, Canola Oil, Soy Protein Isolate, Corn Oil, Soy Fiber, Calcium Phosphate Tribasic, Magnesium Chloride, Potassium Citrate, Cellulose Gel, Soy Lecithin, Potassium Phosphate Dibasic, Sodium Citrate, Natural and Artificial Flavors, Choline Chloride,
- 15 Magnesium Phosphate, Ascorbic Acid, Cellulose Gum, Potassium Chloride, Carrageenan, Ferrous Sulfate, Alpha-Tocopheryl Acetate, Zinc Sulfate, Niacinamide, Manganese Sulfate, Calcium Pantothenate, Cupric Sulfate, Vitamin A Palmitate, Thiamine Chloride Hydrochloride, Pyridoxine Hydrochloride, Riboflavin, Folic Acid, Chromium Chloride, Biotin, Sodium
- 20 Molybdate, Potassium Iodide, Sodium Selenate, Phylloquinone, Vitamin D₃ and Cyanocobalamin.

Protein

The protein source is a blend of two high-biologic-value proteins- casein and soy.

25	Sodium and calcium caseinates	80%
	Soy protein isolate	20%

Fat

The fat source is a blend of three oils: high-oleic safflower, canola, and corn.

	High-oleic safflower oil	40%
5	Canola oil	40%
	Corn oil	20%

The level of fat in ENSURE WITH FIBER meets American Heart Association (AHA) guidelines. The 6 grams of fat in ENSURE WITH FIBER represent 22% of the total calories, with 2.01 % of the fat being from saturated fatty acids and 6.7% from polyunsaturated fatty acids. These values are within the AHA guidelines of $\leq 30\%$ of total calories from fat, $< 10\%$ of the calories from saturated fatty acids, and $\leq 10\%$ of total calories from polyunsaturated fatty acids.

Carbohydrate

ENSURE WITH FIBER contains a combination of maltodextrin and sucrose. The mild sweetness and flavor variety (vanilla, chocolate, and butter pecan), plus VARI-FLAVORS® Flavor Pacs in pecan, cherry, strawberry, lemon, and orange, help to prevent flavor fatigue and aid in patient compliance.

Vanilla and other nonchocolate flavors

20	Maltodextrin	66%
	Sucrose	25%
	Oat Fiber	7%
	Soy Fiber	2%

Chocolate

25	Maltodextrin	55%
	Sucrose	36%
	Oat Fiber	7%

Soy Fiber

2%

Fiber

The fiber blend used in ENSURE WITH FIBER consists of oat fiber and soy polysaccharide. This blend results in approximately 4 grams of total dietary fiber per 8-fl-oz can. The ratio of insoluble to soluble fiber is 95:5.

The various nutritional supplements described above and known to others of skill in the art can be substituted and/or supplemented with the PUFAs of this invention.

J. Oxepa™ Nutritional Product

Oxepa is low-carbohydrate, calorically dense enteral nutritional product designed for the dietary management of patients with or at risk for ARDS. It has a unique combination of ingredients, including a patented oil blend containing eicosapentaenoic acid (EPA from fish oil), γ -linolenic acid (GLA from borage oil), and elevated antioxidant levels.

Caloric Distribution:

- Caloric density is high at 1.5 Cal/mL (355 Cal/8 fl oz), to minimize the volume required to meet energy needs.
- The distribution of Calories in Oxepa is shown in Table 7.

Table 7. Caloric Distribution of Oxepa			
	per 8 fl oz.	per liter	% of Cal
Calories	355	1,500	---
Fat (g)	22.2	93.7	55.2
Carbohydrate (g)	25	105.5	28.1
Protein (g)	14.8	62.5	16.7
Water (g)	186	785	---

Fat:

- Oxepa contains 22.2 g of fat per 8-fl oz serving (93.7 g/L).
- The fat source is a oil blend of 31.8% canola oil, 25% medium-chain triglycerides (MCTs), 20% borage oil, 20% fish oil, and 3.2 % soy lecithin. The typical fatty acid profile of Oxepa is shown in Table 8.

- Oxepa provides a balanced amount of polyunsaturated, monounsaturated, and saturated fatty acids, as shown in Table 10.
- Medium-chain triglycerides (MCTs) -- 25% of the fat blend -- aid gastric emptying because they are absorbed by the intestinal tract without emulsification by bile acids.

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The various fatty acid components of Oxepa™ nutritional product can be substituted and/or supplemented with the PUFAs of this invention.

Table 8. Typical Fatty Acid Profile			
	% Total Fatty Acids	g/8 fl oz*	g/L*
Caproic (6:0)	0.2	0.04	0.18
Caprylic (8:0)	14.69	3.1	13.07
Capric (10:0)	11.06	2.33	9.87
Palmitic (16:0)	5.59	1.18	4.98
Palmitoleic (16:1n-7)	1.82	0.38	1.62
Stearic (18:0)	1.84	0.39	1.64
Oleic (18:1n-9)	24.44	5.16	21.75
Linoleic (18:2n-6)	16.28	3.44	14.49
α -Linolenic (18:3n-3)	3.47	0.73	3.09
γ -Linolenic (18:3n-6)	4.82	1.02	4.29
Eicosapentaenoic (20:5n-3)	5.11	1.08	4.55
n-3-Docosapentaenoic (22:5n-3)	0.55	0.12	0.49
Docosahexaenoic (22:6n-3)	2.27	0.48	2.02
Others	7.55	1.52	6.72

* Fatty acids equal approximately 95% of total fat.

Table 9. Fat Profile of Oxepa.	
% of total calories from fat	55.2
Polyunsaturated fatty acids	31.44 g/L
Monounsaturated fatty acids	25.53 g/L
Saturated fatty acids	32.38 g/L
n-6 to n-3 ratio	1.75:1
Cholesterol	9.49 mg/8 fl oz 40.1 mg/L

Carbohydrate:

- The carbohydrate content is 25.0 g per 8-fl-oz serving (105.5 g/L).
- The carbohydrate sources are 45% maltodextrin (a complex carbohydrate) and 55% sucrose (a simple sugar), both of which are readily digested and absorbed.

• The high-fat and low-carbohydrate content of Oxepa is designed to minimize carbon dioxide (CO₂) production. High CO₂ levels can complicate weaning in ventilator-dependent patients. The low level of carbohydrate also may be useful for those patients who have developed stress-induced hyperglycemia.

- Oxepa is lactose-free.

Dietary carbohydrate, the amino acids from protein, and the glycerol moiety of fats can be converted to glucose within the body. Throughout this process, the carbohydrate requirements of glucose-dependent tissues (such as the central nervous system and red blood cells) are met. However, a diet free of carbohydrates can lead to ketosis, excessive catabolism of tissue protein, and loss of fluid and electrolytes. These effects can be prevented by daily ingestion of 50 to 100 g of digestible carbohydrate, if caloric intake is adequate. The carbohydrate level in Oxepa is also sufficient to minimize gluconeogenesis, if energy needs are being met.

Protein:

- Oxepa contains 14.8 g of protein per 8-fl-oz serving (62.5 g/L).
- The total calorie/nitrogen ratio (150:1) meets the need of stressed patients.
- Oxepa provides enough protein to promote anabolism and the maintenance of lean body mass without precipitating respiratory problems. High protein intakes are a concern in patients with respiratory insufficiency. Although protein has little effect on CO₂ production, a high protein diet will increase ventilatory drive.

- The protein sources of Oxepa are 86.8% sodium caseinate and 13.2% calcium caseinate.
- As demonstrated in Table 11, the amino acid profile of the protein system in Oxepa meets or surpasses the standard for high quality protein set by the National Academy of Sciences.
- Oxepa is gluten-free.

All publications and patent applications mentioned in this specification are indicative of the level of skill of those skilled in the art to which this invention pertains. All publications and patent applications are herein incorporated by reference to the same extent as if each individual publication or patent application was specifically and individually indicated to be incorporated by reference.

The invention now being fully described, it will be apparent to one of ordinary skill in the art that many changes and modifications can be made thereto without departing from the spirit or scope of the appended claims.

SEQUENCE LISTING

5

(1) GENERAL INFORMATION:

(i) APPLICANT: KNUTZON, DEBORAH
MURKERJI, PRADIP
HUANG, YUNG-SHENG
THURMOND, JENNIFER
CHAUDHARY, SUNITA
LEONARD, AMANDA

10

(ii) TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR SYNTHESIS
OF LONG CHAIN POLY-UNSATURATED FATTY ACIDS

15

(iii) NUMBER OF SEQUENCES: 40

(iv) CORRESPONDENCE ADDRESS:

(A) ADDRESSEE: LIMBACH AND LIMBACH LLP
(B) STREET: 2001 FERRY BUILDING
(C) CITY: SAN FRANCISCO
(D) STATE: CA
(E) COUNTRY: USA
(F) ZIP: 94111

20

25

(v) COMPUTER READABLE FORM:

(A) MEDIUM TYPE: Floppy disk
(B) COMPUTER: IBM PC compatible
(C) OPERATING SYSTEM: PC-DOS/MS-DOS
(D) SOFTWARE: Microsoft Word

30

(vi) CURRENT APPLICATION DATA:

(A) APPLICATION NUMBER:
(B) (B) FILING DATE:
(C) CLASSIFICATION:

35

(viii) ATTORNEY/AGENT INFORMATION:

(A) NAME: WARD, MICHAEL R.
(B) REGISTRATION NUMBER: 38,651
(C) REFERENCE/DOCKET NUMBER: CGAB-210

40

(ix) TELECOMMUNICATION INFORMATION:

(A) TELEPHONE: (415) 433-4150
(B) TELEFAX: (415) 433-8716
(C) TELEX: N/A

45

(2) INFORMATION FOR SEQ ID NO:1:

50

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1617 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

55

(ii) MOLECULE TYPE: other nucleic acid

60

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

CGACACTCCT TCCTTCTTCT CACCCGTCCT AGTCCCTTC AACCCCCCTC TTTGACAAAG

60

ACAACAAACC ATGGCTGCTG CTCCAGTGT GAGGACGTTT ACTCGGGCCG AGGTTTGA 120
 TGCCGAGGCT CTGAATGAGG GCAAGAAGGA TGCCGAGGCA CCCTTCTTGA TGATCATCGA 180
 CAACAAGGTG TACGATGTCC GCGAGTTCGT CCCTGATCAT CCCGGTGGAA GTGTGATTCT 240
 CACGCACGTT GGCAAGGACG GCACTGACGT CTTTGACACT TTTCACCCCG AGGCTGCTTG 300
 GGAGACTCTT GCCAACTTTT ACSTTGGTGA TATTGACGAG AGCGACCGCG ATATCAAGAA 360
 TGATGACTTT GCGGCCGAGG TCCGCAAGCT GCGTACCTTG TTCCAGTCTC TTGGTTACTA 420
 CGATTCTTCC AAGGCATACT ACGCCTTCAA GGTCTCGTTC AACCTCTGCA TCTGGGGTTT 480
 GTCGACGGTC ATTGTGGCCA AGTGGGGCCA GACCTCGACC CTCGCCAACG TGCTCTCGGC 540
 TGCCTTTTTG GGTCTGTTCT GGCAGCAGTG CGGATGGTTG GCTCAGACT TTTTGCATCA 600
 CCAGGTCTTC CAGGACCGTT TCTGGGGTGA TCTTTTCGGC GCCTTCTTGG GAGGTGTCTG 660
 CCAGGGCTTC TCGTCCTCGT GGTGGAAGGA CAAGCACAAC ACTCACCACG CCGCCCCCAA 720
 CGTCCACGGC GAGGATCCCG ACATTGACAC CCACCCTCTG TTGACCTGGA GTGAGCATGC 780
 GTTGAGATG TTCTCGGATG TCCCAGATGA GGAGCTGACC CGCATGTGGT CGCGTTTCAT 840
 GGTCTGAAC CAGACCTGGT TTTACTTCCC CATCTCTCG TTTGCCCGTC TCTCCTGGTG 900
 CCTCCAGTCC ATTCTCTTTG TGCTGCCTAA CGGTCAGGCC CACAAGCCCT CGGGCGCGCG 960
 TGTGCCCATC TCGTTGGTCG AGCAGCTGTC GCTTGCGATG CACTGGACCT GGTACCTCGC 1020
 CACCATGTTT CTGTTTCATCA AGGATCCCGT CAACATGCTG GTGTACTTTT TGGTGTGCA 1080
 GGCGGTGTGC GGAAACTTGT TGGCGATCGT GTTCTCGCTC AACCACAACG GTATGCCTGT 1140
 GATCTCGAAG GAGGAGGCGG TCGATATGGA TTTCTTCACG AAGCAGATCA TCACGGGTCG 1200
 TGATGTCCAC CCGGGTCTAT TTGCCAACTG GTTCACGGGT GGATTGAACT ATCAGATCGA 1260
 GCACCACTTG TTCCCTTCGA TGCCTCGCCA CAACTTTTCA AAGATCCAGC CTGCTGTGCA 1320
 GACCCTGTGC AAAAAGTACA ATGTCCGATA CCACACCACC GGTATGATCG AGGGAACGTC 1380
 AGAGGTCTTT AGCCGTCTGA ACGAGGTCTC CAAGGCTGCC TCCAAGATGG GTAAGGCGCA 1440
 GTAAAAAAA AAACAAGGAC GTTTTTTTTC GCCAGTGCCT GTGCCTGTGC CTGCTTCCCT 1500
 TGTCAAGTCG AGCGTTTCTG GAAAGGATCG TTCAGTGCAG TATCATCATT CTCCTTTTAC 1560
 CCCCCGCTCA TATCTCATTC ATTTCTCTTA TTAAACAAC TGTTCCTCCC TTCACCG 1617

(2) INFORMATION FOR SEQ ID NO:2:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 457 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS: not relevant

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

5 Met Ala Ala Ala Pro Ser Val Arg Thr Phe Thr Arg Ala Glu Val Leu
 1 5 10 15
 Asn Ala Glu Ala Leu Asn Glu Gly Lys Lys Asp Ala Glu Ala Pro Phe
 20 25 30
 10 Leu Met Ile Ile Asp Asn Lys Val Tyr Asp Val Arg Glu Phe Val Pro
 35 40 45
 Asp His Pro Gly Gly Ser Val Ile Leu Thr His Val Gly Lys Asp Gly
 50 55 60
 15 Thr Asp Val Phe Asp Thr Phe His Pro Glu Ala Ala Trp Glu Thr Leu
 65 70 75 80
 Ala Asn Phe Tyr Val Gly Asp Ile Asp Glu Ser Asp Arg Asp Ile Lys
 85 90 95
 20 Asn Asp Asp Phe Ala Ala Glu Val Arg Lys Leu Arg Thr Leu Phe Gln
 100 105 110
 25 Ser Leu Gly Tyr Tyr Asp Ser Ser Lys Ala Tyr Tyr Ala Phe Lys Val
 115 120 125
 Ser Phe Asn Leu Cys Ile Trp Gly Leu Ser Thr Val Ile Val Ala Lys
 130 135 140
 30 Trp Gly Gln Thr Ser Thr Leu Ala Asn Val Leu Ser Ala Ala Leu Leu
 145 150 155 160
 Gly Leu Phe Trp Gln Gln Cys Gly Trp Leu Ala His Asp Phe Leu His
 165 170 175
 35 His Gln Val Phe Gln Asp Arg Phe Trp Gly Asp Leu Phe Gly Ala Phe
 180 185 190
 40 Leu Gly Gly Val Cys Gln Gly Phe Ser Ser Ser Trp Trp Lys Asp Lys
 195 200 205
 His Asn Thr His His Ala Ala Pro Asn Val His Gly Glu Asp Pro Asp
 210 215 220
 45 Ile Asp Thr His Pro Leu Leu Thr Trp Ser Glu His Ala Leu Glu Met
 225 230 235 240
 Phe Ser Asp Val Pro Asp Glu Glu Leu Thr Arg Met Trp Ser Arg Phe
 245 250 255
 50 Met Val Leu Asn Gln Thr Trp Phe Tyr Phe Pro Ile Leu Ser Phe Ala
 260 265 270
 55 Arg Leu Ser Trp Cys Leu Gln Ser Ile Leu Phe Val Leu Pro Asn Gly
 275 280 285
 Gln Ala His Lys Pro Ser Gly Ala Arg Val Pro Ile Ser Leu Val Glu
 290 295 300
 60 Gln Leu Ser Leu Ala Met His Trp Thr Trp Tyr Leu Ala Thr Met Phe
 305 310 315 320
 Leu Phe Ile Lys Asp Pro Val Asn Met Leu Val Tyr Phe Leu Val Ser
 325 330 335
 65 Gln Ala Val Cys Gly Asn Leu Leu Ala Ile Val Phe Ser Leu Asn His

340 345 350
 Asn Gly Met Pro Val Ile Ser Lys Glu Glu Ala Val Asp Met Asp Phe
 355 360 365
 5 Phe Thr Lys Gln Ile Ile Thr Gly Arg Asp Val His Pro Gly Leu Phe
 370 375 380
 10 Ala Asn Trp Phe Thr Gly Gly Leu Asn Tyr Gln Ile Glu His His Leu
 385 390 395 400
 Phe Pro Ser Met Pro Arg His Asn Phe Ser Lys Ile Gln Pro Ala Val
 405 410 415
 15 Glu Thr Leu Cys Lys Lys Tyr Asn Val Arg Tyr His Thr Thr Gly Met
 420 425 430
 20 Ile Glu Gly Thr Ala Glu Val Phe Ser Arg Leu Asn Glu Val Ser Lys
 435 440 445
 Ala Ala Ser Lys Met Gly Lys Ala Gln
 450 455

(2) INFORMATION FOR SEQ ID NO:3:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 1488 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

GTCCCCTGTC GCTGTCGGCA CACCCCATCC TCCCTCGCTC CCTCTGCGTT TGTCCCTGGC 60
 CCACCGTCTC TCCTCCACCC TCCGAGACGA CTGCAACTGT AATCAGGAAC CGACAAATAC 120
 ACGATTTCTT TTTACTCAGC ACCAACTCAA AATCCTCAAC CGCAACCCTT TTTCAGGATG 180
 45 GCACCTCCCA ACACTATCGA TGCCGGTTTG ACCCAGCGTC ATATCAGCAC CTCGGCCCCA 240
 AACTCGGCCA AGCCTGCCTT CGAGCGCAAC TACCAGCTCC CCGAGTTCAC CATCAAGGAG 300
 ATCCGAGAGT GCATCCCTGC CCACTGCTTT GAGCGCTCCG GTCTCCGTGG TCTCTGCCAC 360
 50 GTTGCCATCG ATCTGACTTG GGCGTCGCTC TTGTTCTTGG CTGCGACCCA GATCGACAAG 420
 TTTGAGAATC CCTTGATCCG CTATTTGGCC TGGCCTGTTT ACTGGATCAT GCAGGGTATT 480
 55 GTCTGCACCG GTGTCTGGGT GCTGGCTCAC GAGTGTGGTC ATCAGTCCTT CTCGACCTCC 540
 AAGACCCTCA ACAACACAGT TGGTGGATC TTGCACTCGA TGCTCTTGGT CCCCTACCAC 600
 TCCTGGAGAA TCTCGCACTC GAAGCACCAC AAGGCCACTG GCCATATGAC CAAGGACCAG 660
 60 GTCTTTGTGC CCAAGACCCG CTCCCAGGTT GGCTTGCTC CCAAGGAGAA CGCTGCTGCT 720
 GCCGTTCAGG AGGAGGACAT GTCCGTGCAC CTGGATGAGG AGGCTCCCAT TGTGACTTTG 780
 65 TTCTGGATGG TGATCCAGTT CTTGTTCCGA TGGCCCGCGT ACCTGATTAT GAACGCCTCT 840

GGCCAAGACT ACGGCCGCTG GACCTCGCAC TTCCACACGT ACTCGCCCAT CTTTGAGCCC 900
 CGCAACTTTT TCGACATTAT TATCTCGGAC CTCGGTGTGT TGGCTGCCCT CGGTGCCCTG 960
 5 ATCTATGCCT CCATGCAGTT GTCGCTCTTG ACCGTCACCA AGTACTATAT TGTCCCCTAC 1020
 CTCTTTGTCA ACTTTTGGTT GGTCTGTATC ACCTTCTTGC AGCACACCGA TCCCAAGCTG 1080
 10 CCCCATTACC GCGAGGGTGC CTGGAATTTT CAGCGTGGAG CTCTTTGCAC CGTTGACCGC 1140
 TCGTTTGGCA AGTTCTTGA CCATATGTTT CACGGCATTG TCCACACCCA TGTGGCCCAT 1200
 CACTTGTCTT CGCAAATGCC GTTCTACCAT GCTGAGGAAG CTACCTATCA TCTCAAGAAA 1260
 15 CTGCTGGGAG AGTACTATGT GTACGACCCA TCCCGATCG TCGTTGCGGT CTGGAGGTCG 1320
 TTCCGTGAGT GCCGATTCTG GGAGGATCAG GGAGACGTGG TCTTTTCAA GAAGTAAAAA 1380
 AAAAGACAAT GGACCACACA CAACCTTGTC TCTACAGACC TACGTATCAT GTAGCCATAC 1440
 20 CACTTCATAA AAGAACATGA GCTCTAGAGG CGGTGCATTC GCGCCTCC 1488

(2) INFORMATION FOR SEQ ID NO:4:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 399 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: not relevant
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

Met Ala Pro Pro Asn Thr Ile Asp Ala Gly Leu Thr Gln Arg His Ile
 1 5 10 15
 Ser Thr Ser Ala Pro Asn Ser Ala Lys Pro Ala Phe Glu Arg Asn Tyr
 20 25 30
 Gln Leu Pro Glu Phe Thr Ile Lys Glu Ile Arg Glu Cys Ile Pro Ala
 35 40 45
 His Cys Phe Glu Arg Ser Gly Leu Arg Gly Leu Cys His Val Ala Ile
 50 55 60
 Asp Leu Thr Trp Ala Ser Leu Leu Phe Leu Ala Ala Thr Gln Ile Asp
 65 70 75 80
 Lys Phe Glu Asn Pro Leu Ile Arg Tyr Leu Ala Trp Pro Val Tyr Trp
 85 90 95
 Ile Met Gln Gly Ile Val Cys Thr Gly Val Trp Val Leu Ala His Glu
 100 105 110
 Cys Gly His Gln Ser Phe Ser Thr Ser Lys Thr Leu Asn Asn Thr Val
 115 120 125
 Gly Trp Ile Leu His Ser Met Leu Leu Val Pro Tyr His Ser Trp Arg
 130 135 140
 65 Ile Ser His Ser Lys His His Lys Ala Thr Gly His Met Thr Lys Asp
 145 150 155 160

5 Gln Val Phe Val Pro Lys Thr Arg Ser Gln Val Gly Leu Pro Pro Lys
 165 170 175
 Glu Asn Ala Ala Ala Val Gln Glu Glu Asp Met Ser Val His Leu
 180 185 190
 10 Asp Glu Glu Ala Pro Ile Val Thr Leu Phe Trp Met Val Ile Gln Phe
 195 200 205
 Leu Phe Gly Trp Pro Ala Tyr Leu Ile Met Asn Ala Ser Gly Gln Asp
 210 215 220
 15 Tyr Gly Arg Trp Thr Ser His Phe His Thr Tyr Ser Pro Ile Phe Glu
 225 230 235 240
 Pro Arg Asn Phe Phe Asp Ile Ile Ile Ser Asp Leu Gly Val Leu Ala
 245 250 255
 20 Ala Leu Gly Ala Leu Ile Tyr Ala Ser Met Gln Leu Ser Leu Leu Thr
 260 265 270
 Val Thr Lys Tyr Tyr Ile Val Pro Tyr Leu Phe Val Asn Phe Trp Leu
 275 280 285
 25 Val Leu Ile Thr Phe Leu Gln His Thr Asp Pro Lys Leu Pro His Tyr
 290 295 300
 Arg Glu Gly Ala Trp Asn Phe Gln Arg Gly Ala Leu Cys Thr Val Asp
 305 310 315 320
 Arg Ser Phe Gly Lys Phe Leu Asp His Met Phe His Gly Ile Val His
 325 330 335
 30 Thr His Val Ala His His Leu Phe Ser Gln Met Pro Phe Tyr His Ala
 340 345 350
 Glu Glu Ala Thr Tyr His Leu Lys Lys Leu Leu Gly Glu Tyr Tyr Val
 355 360 365
 35 Tyr Asp Pro Ser Pro Ile Val Val Ala Val Trp Arg Ser Phe Arg Glu
 370 375 380
 Cys Arg Phe Val Glu Asp Gln Gly Asp Val Val Phe Phe Lys Lys
 385 390 395

(2) INFORMATION FOR SEQ ID NO:5:

50 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 355 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: not relevant
 (D) TOPOLOGY: linear

55 (ii) MOLECULE TYPE: peptide

60 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

Glu Val Arg Lys Leu Arg Thr Leu Phe Gln Ser Leu Gly Tyr Tyr Asp
 1 5 10 15
 Ser Ser Lys Ala Tyr Tyr Ala Phe Lys Val Ser Phe Asn Leu Cys Ile
 20 25 30

Trp Gly Leu Ser Thr Val Ile Val Ala Lys Trp Gly Gln Thr Ser Thr
 35 40 45
 5 Leu Ala Asn Val Leu Ser Ala Ala Leu Leu Gly Leu Phe Trp Gln Gln
 50 55 60
 Cys Gly Trp Leu Ala His Asp Phe Leu His His Gln Val Phe Gln Asp
 65 70 75 80
 10 Arg Phe Trp Gly Asp Leu Phe Gly Ala Phe Leu Gly Gly Val Cys Gln
 85 90 95
 Gly Phe Ser Ser Ser Trp Trp Lys Asp Lys His Asn Thr His His Ala
 100 105 110
 15 Ala Pro Asn Val His Gly Glu Asp Pro Asp Ile Asp Thr His Pro Leu
 115 120 125
 20 Leu Thr Trp Ser Glu His Ala Leu Glu Met Phe Ser Asp Val Pro Asp
 130 135 140
 Glu Glu Leu Thr Arg Met Trp Ser Arg Phe Met Val Leu Asn Gln Thr
 145 150 155 160
 25 Trp Phe Tyr Phe Pro Ile Leu Ser Phe Ala Arg Leu Ser Trp Cys Leu
 165 170 175
 Gln Ser Ile Leu Phe Val Leu Pro Asn Gly Gln Ala His Lys Pro Ser
 180 185 190
 30 Gly Ala Arg Val Pro Ile Ser Leu Val Glu Gln Leu Ser Leu Ala Met
 195 200 205
 35 His Trp Thr Trp Tyr Leu Ala Thr Met Phe Leu Phe Ile Lys Asp Pro
 210 215 220
 Val Asn Met Leu Val Tyr Phe Leu Val Ser Gln Ala Val Cys Gly Asn
 225 230 235 240
 40 Leu Leu Ala Ile Val Phe Ser Leu Asn His Asn Gly Met Pro Val Ile
 245 250 255
 Ser Lys Glu Glu Ala Val Asp Met Asp Phe Phe Thr Lys Gln Ile Ile
 260 265 270
 Thr Gly Arg Asp Val His Pro Gly Leu Phe Ala Asn Trp Phe Thr Gly
 275 280 285
 50 Gly Leu Asn Tyr Gln Ile Glu His His Leu Phe Pro Ser Met Pro Arg
 290 295 300
 His Asn Phe Ser Lys Ile Gln Pro Ala Val Glu Thr Leu Cys Lys Lys
 305 310 315 320
 55 Tyr Asn Val Arg Tyr His Thr Thr Gly Met Ile Glu Gly Thr Ala Glu
 325 330 335
 Val Phe Ser Arg Leu Asn Glu Val Ser Lys Ala Ala Ser Lys Met Gly
 340 345 350
 Lys Ala Gln
 355

(2) INFORMATION FOR SEQ ID NO:6:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 104 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: not relevant
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

Val Thr Leu Tyr Thr Leu Ala Phe Val Ala Ala Asn Ser Leu Gly Val
 1 5 10 15
 Leu Tyr Gly Val Leu Ala Cys Pro Ser Val Xaa Pro His Gln Ile Ala
 20 25 30
 Ala Gly Leu Leu Gly Leu Leu Trp Ile Gln Ser Ala Tyr Ile Gly Xaa
 35 40 45
 Asp Ser Gly His Tyr Val Ile Met Ser Asn Lys Ser Asn Asn Xaa Phe
 50 55 60
 Ala Gln Leu Leu Ser Gly Asn Cys Leu Thr Gly Ile Ile Ala Trp Trp
 65 70 75 80
 Lys Trp Thr His Asn Ala His His Leu Ala Cys Asn Ser Leu Asp Tyr
 85 90 95
 Gly Pro Asn Leu Gln His Ile Pro
 100

(2) INFORMATION FOR SEQ ID NO:7:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 252 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: not relevant
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

Gly Val Leu Tyr Gly Val Leu Ala Cys Thr Ser Val Phe Ala His Gln
 1 5 10 15
 Ile Ala Ala Ala Leu Leu Gly Leu Leu Trp Ile Gln Ser Ala Tyr Ile
 20 25 30
 Gly His Asp Ser Gly His Tyr Val Ile Met Ser Asn Lys Ser Tyr Asn
 35 40 45
 Arg Phe Ala Gln Leu Leu Ser Gly Asn Cys Leu Thr Gly Ile Ser Ile
 50 55 60
 Ala Trp Trp Lys Trp Thr His Asn Ala His His Leu Ala Cys Asn Ser
 65 70 75 80
 Leu Asp Tyr Asp Pro Asp Leu Gln His Ile Pro Val Phe Ala Val Ser
 85 90 95

Thr Lys Phe Phe Ser Ser Leu Thr Ser Arg Phe Tyr Asp Arg Lys Leu
 100 105 110
 5 Thr Phe Gly Pro Val Ala Arg Phe Leu Val Ser Tyr Gln His Phe Thr
 115 120 125
 Tyr Tyr Pro Val Asn Cys Phe Gly Arg Ile Asn Leu Phe Ile Gln Thr
 130 135 140
 10 Phe Leu Leu Leu Phe Ser Lys Arg Glu Val Pro Asp Arg Ala Leu Asn
 145 150 155 160
 Phe Ala Gly Ile Leu Val Phe Trp Thr Trp Phe Pro Leu Leu Val Ser
 165 170 175
 15 Cys Leu Pro Asn Trp Pro Glu Arg Phe Phe Phe Val Phe Thr Ser Phe
 180 185 190
 20 Thr Val Thr Ala Leu Gln His Ile Gln Phe Thr Leu Asn His Phe Ala
 195 200 205
 Ala Asp Val Tyr Val Gly Pro Pro Thr Gly Ser Asp Trp Phe Glu Lys
 210 215 220
 25 Gln Ala Ala Gly Thr Ile Asp Ile Ser Cys Arg Ser Tyr Met Asp Trp
 225 230 235 240
 Phe Phe Gly Gly Leu Gln Phe Gln Leu Glu His His
 245 250
 30

(2) INFORMATION FOR SEQ ID NO:8:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 125 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: not relevant
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

Gly Xaa Xaa Asn Phe Ala Gly Ile Leu Val Phe Trp Thr Trp Phe Pro
 1 5 10 15
 50 Leu Leu Val Ser Cys Leu Pro Asn Trp Pro Glu Arg Phe Xaa Phe Val
 20 25 30
 Phe Thr Gly Phe Thr Val Thr Ala Leu Gln His Ile Gln Phe Thr Leu
 35 40 45
 55 Asn His Phe Ala Ala Asp Val Tyr Val Gly Pro Pro Thr Gly Ser Asp
 50 55 60
 60 Trp Phe Glu Lys Gln Ala Ala Gly Thr Ile Asp Ile Ser Cys Arg Ser
 65 70 75 80
 Tyr Met Asp Trp Phe Phe Cys Gly Leu Gln Phe Gln Leu Glu His His
 85 90 95
 65 Leu Phe Pro Arg Leu Pro Arg Cys His Leu Arg Lys Val Ser Pro Val
 100 105 110

Gly Gln Arg Gly Phe Gln Arg Lys Xaa Asn Leu Ser Xaa
 115 120 125

5 (2) INFORMATION FOR SEQ ID NO:9:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 131 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: not relevant
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

Pro Ala Thr Glu Val Gly Gly Leu Ala Trp Met Ile Thr Phe Tyr Val
 1 5 10 15
 Arg Phe Phe Leu Thr Tyr Val Pro Leu Leu Gly Leu Lys Ala Phe Leu
 20 25 30
 Gly Leu Phe Phe Ile Val Arg Phe Leu Glu Ser Asn Trp Phe Val Trp
 35 40 45
 Val Thr Gln Met Asn His Ile Pro Met His Ile Asp His Asp Arg Asn
 50 55 60
 Met Asp Trp Val Ser Thr Gln Leu Gln Ala Thr Cys Asn Val His Lys
 65 70 75 80
 Ser Ala Phe Asn Asp Trp Phe Ser Gly His Leu Asn Phe Gln Ile Glu
 85 90 95
 His His Leu Phe Pro Thr Met Pro Arg His Asn Tyr His Xaa Val Ala
 100 105 110
 Pro Leu Val Gln Ser Leu Cys Ala Lys His Gly Ile Glu Tyr Gln Ser
 115 120 125
 Lys Pro Leu
 130

(2) INFORMATION FOR SEQ ID NO:10:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 87 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: not relevant
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

Cys Ser Pro Lys Ser Ser Pro Thr Arg Asn Met Thr Pro Ser Pro Phe
 1 5 10 15
 Ile Asp Trp Leu Trp Gly Gly Leu Asn Tyr Gln Ile Glu His His Leu
 20 25 30

Phe Pro Thr Met Pro Arg Cys Asn Leu Asn Arg Cys Met Lys Tyr Val
35 40 45

5 Lys Glu Trp Cys Ala Glu Asn Asn Leu Pro Tyr Leu Val Asp Asp Tyr
50 55 60

10 Phe Val Gly Tyr Asn Leu Asn Leu Gln Gln Leu Lys Asn Met Ala Glu
65 70 75 80

10 Leu Val Gln Ala Lys Ala Ala
85

15 (2) INFORMATION FOR SEQ ID NO:11:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 143 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: not relevant
(D) TOPOLOGY: linear

20 (ii) MOLECULE TYPE: peptide

25 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:

30 Arg His Glu Ala Ala Arg Gly Gly Thr Arg Leu Ala Tyr Met Leu Val
1 5 10 15

Cys Met Gln Trp Thr Asp Leu Leu Trp Ala Ala Ser Phe Tyr Ser Arg
20 25 30

35 Phe Phe Leu Ser Tyr Ser Pro Phe Tyr Gly Ala Thr Gly Thr Leu Leu
35 40 45

40 Leu Phe Val Ala Val Arg Val Leu Glu Ser His Trp Phe Val Trp Ile
50 55 60

Thr Gln Met Asn His Ile Pro Lys Glu Ile Gly His Glu Lys His Arg
65 70 75 80

45 Asp Trp Ala Ser Ser Gln Leu Ala Ala Thr Cys Asn Val Glu Pro Ser
85 90 95

Leu Phe Ile Asp Trp Phe Ser Gly His Leu Asn Phe Gln Ile Glu His
100 105 110

50 His Leu Phe Pro Thr Met Thr Arg His Asn Tyr Arg Xaa Val Ala Pro
115 120 125

55 Leu Val Lys Ala Phe Cys Ala Lys His Gly Leu His Tyr Glu Val
130 135 140

(2) INFORMATION FOR SEQ ID NO:12:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 35 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:12:

5 CCAAGCTTCT GCAGGAGCTC TTTTTTTTTT TTTT 35

(2) INFORMATION FOR SEQ ID NO:13:

10 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 33 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

15 (ii) MOLECULE TYPE: other nucleic acid

20 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:13:

CUACUACUAC UAGGAGTCCT CTACGGTGTT TTG 33

25 (2) INFORMATION FOR SEQ ID NO:14:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 33 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

35 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:14:

40 CAUCAUCAUC AUATGATGCT CAAGCTGAAA CTG 33

(2) INFORMATION FOR SEQ ID NO:15:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 39 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

50 (ii) MOLECULE TYPE: other nucleic acid

55 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:15:

TACCAACTCG AGAAAATGGC TGCTGCTCCC AGTGTGAGG 39

(2) INFORMATION FOR SEQ ID NO:16:

60 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 39 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

65 (ii) MOLECULE TYPE: other nucleic acid

5 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:16:

AACTGATCTA GATTACTGCG CCTTACCCAT CTTGGAGGC

39

(2) INFORMATION FOR SEQ ID NO:17:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 39 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:17:

TACCAACTCG AGAAAATGGC ACCTCCCAAC ACTATCGAT

39

(2) INFORMATION FOR SEQ ID NO:18:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 39 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:18:

AACTGATCTA GATTACTTCT TGAAAAGAC CACGTCTCC

39

(2) INFORMATION FOR SEQ ID NO:19:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 746 nucleic acids
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: not relevant
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: nucleic acid

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:19:

CGTATGTCAC	TCCATTCCAA	ACTCGTTCAT	GGTATCATAA	ATATCAACAC	ATTTACGCTC	60
CACTCCTCTA	TGGTATTTAC	ACACTCAAAT	ATCGTACTCA	AGATTGGGAA	GCTTTTGTAA	120
AGGATGGTAA	AAATGGTGCA	ATTCTGTGTA	GTGTCGCCAC	AAATTCGAT	AAGGCCGCTT	180
ACGTCATGCG	TAAATTGTCT	TTTGTTTCT	TCCGTTTCAT	CCTTCCACTC	CGTTATCATA	240
GCTTTACAGA	TTTAATTTGT	TATTTCTCA	TGCTGAATT	CGTCTTGGT	TGGTATCTCA	300
CAATTAATTT	CCAAGTTAGT	CATGTCGCTG	AAGATCTCAA	ATTCTTTGCT	ACCCCTGAAA	360
GACCAGATGA	ACCATCTCAA	ATCAATGAAG	ATTGGGCAAT	CCTTCAACTT	AAAACACTC	420
AAGATTATGG	TCATGGTTCA	CTCCTTTGTA	CCTTTTITAG	TGGTTCCTTA	AATCATCAAG	480
TTGTTTCATCA	TTTATTCCCA	TCAATTGCTC	AAGATTTCTA	CCCACAACTT	GTACCAATTG	540
TAAAAGAAGT	TTGTAAAGAA	CATAACATTA	CTTACCACAT	TAAACCAAAC	TTCACCTGAAG	600
CTATTATGTC	ACACATTAAT	TACCTTTACA	AAATGGGTAA	TGATCCAGAT	TATGTTAAAA	660
AACCATTAGC	CTCAAAAGAT	GATTAAATGA	AATAACTTAA	AAACCAATTA	TTTACTTTTG	720

ACAAACAGTA ATATTAATAA ATACAA

746

(2) INFORMATION FOR SEQ ID NO:20:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 227 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: not relevant
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:20:

Tyr Val Thr Pro Phe Gln Thr Arg Ser Trp Tyr His Lys Tyr Gln
 1 5 10 15
 His Ile Tyr Ala Pro Leu Leu Tyr Gly Ile Tyr Thr Leu Lys Tyr
 20 25 30
 Arg Thr Gln Asp Trp Glu Ala Phe Val Lys Asp Gly Lys Asn Gly
 35 40 45
 Ala Ile Arg Val Ser Val Ala Thr Asn Phe Asp Lys Ala Ala Tyr
 50 55 60
 Val Ile Gly Lys Leu Ser Phe Val Phe Phe Arg Phe Ile Leu Pro
 65 70 75
 Leu Arg Tyr His Ser Phe Thr Asp Leu Ile Cys Tyr Phe Leu Ile
 80 85 90
 Ala Glu Phe Val Phe Gly Trp Tyr Leu Thr Ile Asn Phe Gln Val
 95 100 105
 Ser His Val Ala Glu Asp Leu Lys Phe Phe Ala Thr Pro Glu Arg
 110 115 120
 Pro Asp Glu Pro Ser Gln Ile Asn Glu Asp Trp Ala Ile Leu Gln
 125 130 135
 Leu Lys Thr Thr Gln Asp Tyr Gly His Gly Ser Leu Leu Cys Thr
 140 145 150
 Phe Phe Ser Gly Ser Leu Asn His Gln Val Val His His Leu Phe
 155 160 165
 Pro Ser Ile Ala Gln Asp Phe Tyr Pro Gln Leu Val Pro Ile Val
 170 175 180
 Lys Glu Val Cys Lys Glu His Asn Ile Thr Tyr His Ile Lys Pro
 185 190 195
 Asn Phe Thr Glu Ala Ile Met Ser His Ile Asn Tyr Leu Tyr Lys
 200 205 210
 Met Gly Asn Asp Pro Asp Tyr Val Lys Lys Pro Leu Ala Ser Lys
 215 220 225
 Asp Asp ***

(2) INFORMATION FOR SEQ ID NO 21:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 494 nucleic acids
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: not relevant
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: nucleic acid

(xi) SEQUENCE DESCRIPTION:SEQ ID NO:21:

TTTGGAAGG NTCCAAGTTN ACCACGGANT NGGCAAGTTN ACGGGGCGGA AANCGGTTTT 60
 CCCCCAAGC CTTTTGTCGA CTGGTTCTGT GGTGGCTTCC AGTACCAAGT CGACCACCAC 120
 TTATCCCCA GCCTGCCCGG ACACAATCTG GCCAAGACAC ACGCACTGGT CGAATCGTTC 180
 TGCAAGGAGT GGGGTGTCCA GTACCACGAA GCCGACCTCG TGGACGGGAC CATGGAAGTC 240
 TTGACCAATT TGGGCAGCGT GGCCGGCGAA TTCGTCGTGG ATTTTGTACG CGACGGACCC 300

GCCATGTAAT CGTCGTTCGT GACGATGCAA GGGTTCACGC ACATCTACAC AACTCACTC 360
 ACACAACTAG TGTAACCTCGT ATAGAATTCG GTGTCGACCT GGACCTTGTT TGA CTGGTTG 420
 GGGATAGGGT AGGTAGGCGG ACGCGTGGGT CGNCCCCGGG AATTCTGTGA CCGGTACCTG 480
 GCCCGCGTNA AAGT 494

(2) INFORMATION FOR SEQ ID NO:22:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 87 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: not relevant
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:22:

Phe Trp Lys Xxx Pro Ser Xxx Pro Arg Xxx Xxx Gln Val Xxx Gly
 1 5 10 15
 Ala Glu Xxx Gly Phe Pro Pro Lys Pro Phe Val Asp Trp Phe Cys
 20 25 30
 Gly Gly Phe Gln Tyr Gln Val Asp His His Leu Phe Pro Ser Leu
 35 40 45
 Pro Arg His Asn Leu Ala Lys Thr His Ala Leu Val Glu Ser Phe
 50 55 60
 Cys Lys Glu Trp Gly Val Gln Tyr His Glu Ala Asp Leu Val Asp
 65 70 75
 Gly Thr Met Glu Val Leu His His Leu Gly Ser Val Ala Gly Glu
 80 85
 Phe Val Val Asp Phe Val Arg Asp Gly Pro Ala Met

(2) INFORMATION FOR SEQ ID NO:23:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 520 nucleic acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: not relevant
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: nucleic acid

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:23:

GGATGGAGTT CGTCTGGATC GCTGTGCGCT ACGCGACGTG GTTTAAGCGT CATGGGTGCG 60
 CTTGGGTACA CGCCGGGGCA GTCGTTGGGC ATGTA CTGTG GCGCCTTTGG TCTCGGCTGC 120
 ATTTACATTT TTCTGCAGTT CGCCGTAAGT CACACCCATT TGCCCGTGAG CAACCCGGAG 180
 GATCAGCTGC ATTGGCTCGA GTACGCGCGG ACCACACTGT GAACATCAGC ACCAAGTCGT 240
 GGT TTGTG CAC ATGGTGGATG TCGAACCTCA ACTTTCAGAT CGAGCACCAC CTTTCCCCCA 300
 CGGCGCCCCA GTTCCGTTTC AAGGAGATCA GCCCGCGCGT CGAGGCCCTC TTCAAGCGCC 360
 ACGGTCTCCC TTA CTACGAC ATGCCCTACA CGAGCGCCGT CTCCACCACC TTTGCCAACC 420
 TCTACTCCGT CGGCCATTCC GTCGGCGACG CCAAGCGCGA CTAGCCTCTT TTCCTAGACC 480
 TTAATTCCCC ACCCCACCCC ATGTTCTGTC TTCCTCCGCG 520

(2) INFORMATION FOR SEQ ID NO:24:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 153 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: not relevant
 (D) TOPOLOGY: linear

5

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:24:

10

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Met Glu Phe Val Trp Ile Ala Val Arg Tyr Ala Thr Trp Phe Lys
1      5      10      15
Arg His Gly Cys Ala Trp Val His Ala Gly Ala Val Val Gly His
20      25      30
Val Leu Val Arg Leu Trp Ser Arg Leu His Leu His Phe Ser Ala
35      40      45
Val Arg Arg Lys Ser His Pro Phe Ala Arg Glu Gln Pro Gly Gly
50      55      60
Ser Ala Ala Leu Ala Arg Val Arg Ala Asp His Thr Val Asn Ile
20      65      70      75
Ser Thr Lys Ser Trp Phe Val Thr Trp Trp Met Ser Asn Leu Asn
80      85      90
Phe Gln Ile Glu His His Leu Phe Pro Thr Ala Pro Gln Phe Arg
95      100      105
Phe Lys Glu Ile Ser Pro Arg Val Glu Ala Leu Phe Lys Arg His
25      110      115      120
Gly Leu Pro Tyr Tyr Asp Met Pro Tyr Thr Ser Ala Val Ser Thr
125      130      135
Thr Phe Ala Asn Leu Tyr Ser Val Gly His Ser Val Gly Asp Ala
30      140      145      150
Lys Arg Asp

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35

(2) INFORMATION FOR SEQ ID NO:25:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 420 nucleic acids
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: not relevant
 (D) TOPOLOGY: linear

40

(ii) MOLECULE TYPE: nucleic acid

45

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:25:

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ACGCGTCCGC CCACGCGTCC GCCGCGAGCA ACTCATCAAG GAAGGCTACT TTGACCCCTC      60
GCTCCCGCAC ATGACGTACC GCGTGGTCTGA GATTGTTGTT CTCTTCGTGC TTTCCTTTTG      120
GCTGATGGGT CAGTCTTCAC CCTCGCGCT CGCTCTCGGC ATTGTCGTCA GCGGCATCTC      180
TCAGGGTCGC TGC GGCTGGG TAATGCATGA GATGGGCCAT GGGTCGTTCA CTGGTGTCAT      240
TTGGCTTGAC GACCGTTGT GCGAGTTCTT TTACGGCGTT GGTGTGGCA TGAGCGGTCA      300
TTACTGGAAA AACCAGCACA GCAAACACCA CGCAGCGCCA AACC GGCTCG AGCACGATGT      360
AGATCTCAAC ACCTTGCCAT TGGTGGCCTT CAACGAGCGC GTCGTGCGCA AGGTCCGACC      420

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55

(2) INFORMATION FOR SEQ ID NO:26:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 125 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: not relevant
 (D) TOPOLOGY: linear

60

(ii) MOLECULE TYPE: peptide

65

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:26:

5 Arg Val Arg Pro Arg Val Arg Arg Glu Gln Leu Ile Lys Glu Gly
 1 5 10 15
 Tyr Phe Asp Pro Ser Leu Pro His Met Thr Tyr Arg Val Val Glu
 20 25 30
 10 Ile Val Val Leu Phe Val Leu Ser Phe Trp Leu Met Gly Gln Ser
 35 40 45
 Ser Pro Leu Ala Leu Ala Leu Gly Ile Val Val Ser Gly Ile Ser
 50 55 60
 Gln Gly Arg Cys Gly Trp Val Met His Glu Met Gly His Gly Ser
 65 70 75
 15 Phe Thr Gly Val Ile Trp Leu Asp Asp Arg Leu Cys Glu Phe Phe
 65 70 75
 Tyr Gly Val Gly Cys Gly Met Ser Gly His Tyr Trp Lys Asn Gln
 80 85 90
 20 His Ser Lys His His Ala Ala Pro Asn Arg Leu Glu His Asp Val
 95 100 105
 Asp Leu Asn Thr Leu Pro Leu Val Ala Phe Asn Glu Arg Val Val
 110 115 120
 Arg Lys Val Arg Pro
 125

(2) INFORMATION FOR SEQ ID NO:27:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1219 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid (Edited Contig 2692004)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:27:

40 GCACGCCGAC CGGCGCCGGG AGATCCTGGC AAAGTATCCA GAGATAAAGT CCTTGATGAA 60
 ACCTGATCCC AATTTGATAT GGATTATAAT TATGATGGTT CTCACCCAGT TGGGTGCATT 120
 45 TTACATAGTA AAAGACTTGG ACTGGAAATG GGTCATATTT GGGGCCTATG CGTTTGGCAG 180
 TTGCATTAAC CACTCAATGA CTCTGGCTAT TCATGAGATT GCCCACAATG CTGCCTTTGG 240
 CAACTGCAAA GCAATGTGGA ATCGCTGGTT TGGAATGTTT GCTAATCTTC CTATTGGGAT 300
 50 TCCATATTCA ATTTCTTTTA AGAGGTATCA CATGGATCAT CATCGGTACC TTGGAGCTGA 360
 TGGCGTCGAT GTAGATATTC CTACCGATTT TGAGGGCTGG TTCTTCTGTA CCGCTTTTCAG 420
 55 AAAGTTTATA TGGGTTATTC TTCAGCCTCT CTTTATGCC TTTCGACCTC TGTTCATCAA 480
 CCCCAAACCA ATTACGTATC TGAAGTTAT CAATACCGTG GCACAGGTCA CTTTGGACAT 540
 TTTAATTTAT TACTTTTTGG GAATTAAATC CTTAGTCTAC ATGTTGGCAG CATCTTTACT 600
 60 TGGCCTGGGT TTGCACCCAA TTTCTGGACA TTTTATAGCT GAGCATTACA TGTCTTAA 660
 GGGTCATGAA ACTTACTCAT ATTATGGGCC TCTGAATTTA CTTACCTTCA ATGTGGGTTA 720
 TCATAATGAA CATCATGATT TCCCCAACAT TCCTGGAAAA AGTCTTCCAC TGGTGAGGAA 780
 65 AATAGCAGCT GAATACTATG ACAACCTCCC TCACTACAAT TCCTGGATAA AAGTACTGTA 840

5 TGATTTTGTG ATGGATGATA CAATAAGTCC CTAACAAGA ATGAAGAGGC ACCAAAAAGG 900
 AGAGATGGTG CTGGAGTAAA TATCATTAGT GCCAAAGGGA TTCTTCTCCA AACTTTTAGA 960
 TGATAAAATG GAATTTTGTG ATTATTAAAC TTGAGACCAG TGATGCTCAG AAGCTCCCCT 1020
 GGCACAATTT CAGAGTAAGA GCTCGGTGAT ACCAAGAAGT GAATCTGGCT TTAAACAGT 1080
 10 CAGCCTGACT CTGTACTGCT CAGTTTCACT CACAGGAAAC TTGTGACTTG TGTATTATCG 1140
 TCATTGAGGA TGTTTCACTC ATGTCTGTCA TTTTATAAGC ATATCATTTA AAAAGCTTCT 1200
 15 AAAAAGCTAT TTCGCCAGG 1219

(2) INFORMATION FOR SEQ ID NO:28:

- 20 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 655 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

25 (ii) MOLECULE TYPE: other nucleic acid (Edited Contig 2153526)

30 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:28:

35 TTACCTTCTA CGTCCGCTTC TTCCTCACTT ATGTGCCACT ATTGGGGCTG AAAGCTTCCT 60
 GGGCCTTTTC TTCATAGTCA GGTTCCTGGA AAGCAACTGG TTTGTGTGGG TGACACAGAT 120
 GAACCATATT CCCATGCACA TTGATCATGA CCGGAACATG GACTGGGTTT CCACCCAGCT 180
 CCAGGCCACA TGCAATGTCC ACAAGTCTGC CTTCAATGAC TGGTTCAGTG GACACCTCAA 240
 40 CTTCCAGATT GAGCACCATC TTTTCCAC GATGCCTCGA CACAATTACC ACAAGTGGC 300
 TCCCCTGGTG CAGTCCTTGT GTGCCAAGCA TGGCATAGAG TACCACTCCA AGCCCTGCT 360
 GTCAGCCTTC GCCGACATCA TCCACTCACT AAAGGAGTCA GGGCAGCTCT GGCTAGATGC 420
 45 CTATCTTCAC CAATAACAAC AGCCACCCTG CCCAGTCTGG AAGAAGAGGA GGAAGACTCT 480
 GGAGCCAAGG CAGAGGGGAG CTTGAGGGAC AATGCCACTA TAGTTTAATA CTCAGAGGGG 540
 50 GTTGGGTTTG GGGACATAAA GCCTCTGACT CAAACTCCTC CCTTTTATCT TCTAGCCACA 600
 GTTCTAAGAC CCAAAGTGGG GGGTGGACAC AGAAGTCCCT AGGAGGGAAG GAGCT 655

55 (2) INFORMATION FOR SEQ ID NO:29:

- 60 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 304 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid (Edited Contig 3506132)

65 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:29:

GTCTTTTACT TTGGCAATGG CTGGATTCCT ACCCTCATCA CGGCCTTGT CCTTGCTACC 60

TCTCAGGCCC AAGCTGGATG GCTGCAACAT GATTATGGCC ACCTGTCTGT CTACAGAAAA 120
 CCCAAGTGGA ACCACCTTGT CCACAAATTC GTCATTGGCC ACTTAAAGGG TGCCTCTGCC 180
 AACTGGTGGA ATCATCGCCA CTTCCAGCAC CACGCCAAGC CTAACATCTT CCACAAGGAT 240
 CCCGATGTGA ACATGCTGCA CGTGTGTTGTT CTGGGCGAAT GGCAGCCCAT CGAGTACGGC 300
 AAGA 304

(2) INFORMATION FOR SEQ ID NO:30:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 918 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid (Edited Contig 3854933)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:30:

CAGGGACCTA CCCGCGCTA CTTACCTGG GACGAGGTGG CCCAGCGCTC AGGGTGCAG 60
 GAGCGGTGGC TAGTGATCGA CCGTAAGGTG TACAACATCA GCGAGTTCAC CCGCCGGCAT 120
 CCAGGGGGCT CCCGGGTCAT CAGCCACTAC GCCGGGCAGG ATGCCACGGA TCCCTTTGTG 180
 GCCTTCCACA TCAACAAGGG CCTTGTGAAG AAGTATATGA ACTCTCTCCT GATTGGAGAA 240
 CTGTCTCCAG AGCAGCCCAG CTTTGAGCCC ACCAAGAATA AAGAGCTGAC AGATGAGTTC 300
 CGGGAGCTGC GGGCCACAGT GGAGCGGATG GGGCTCATGA AGGCCAACCA TGTCTTCTTC 360
 CTGCTGTACC TGCTGCACAT CTGCTGCTG GATGGTGCAG CCTGGCTCAC CCTTTGGGTC 420
 TTTGGGACGT CCTTTTGGCC CTTCCTCCTC TGTGCGGTGC TGCTCAGTGC AGTTCAGGCC 480
 CAGGCTGGCT GGCTGCAGCA TGACTTTGGG CACCTGTCGG TCTTCAGCAC CTCAAAGTGG 540
 AACCATCTGC TACATCATTT TGTGATTGGC CACCTGAAGG GGGCCCCCGC CAGTTGGTGG 600
 AACCACATGC ACTTCCAGCA CCATGCCAAG CCCAACTGCT TCCGCAAAGA CCCAGACATC 660
 AACATGCATC CCTTCTTCTT TGCCTTGGGG AAGATCCTCT CTGTGGAGCT TGGGAAACAG 720
 AAGAAAAAAT ATATGCCGTA CAACCACCAG CACARATACT TCTTCCTAAT TGGGCCCCCA 780
 GCCTTGCTGC CTCTCTACTT CCAGTGGTAT ATTTTCTATT TTGTTATCCA GCGAAAGAAG 840
 TGGGTGGACT TGGCCTGGAT CAGCAAACAG GAATACGATG AAGCCGGGCT TCCATTGTCC 900
 ACCGCAAATG CTTCTAAA 918

(2) INFORMATION FOR SEQ ID NO:31:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 1686 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid (Edited Contig 2511785)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:31:

5 GCCACTTAAA GGGTGCCTCT GCCAACTGGT GGAATCATCG CCACTTCCAG CACCACGCCA 60
 AGCCTAACAT CTTCCACAAG GATCCCGATG TGAACATGCT GCACGTGTTT GTTCTGGGCG 120
 10 AATGGCAGCC CATCGAGTAC GGCAAGAAGA AGCTGAAATA CCTGCCCTAC AATCACCAGC 180
 ACGAATACTT CTTCCTGATT GGGCCGCCGC TGCTCATCCC CATGTATTTT CAGTACCAGA 240
 TCATCATGAC CATGATCGTC CATAAGAACT GGGTGGACCT GGCCTGGGCC GTCAGCTACT 300
 15 ACATCCGGTT CTTTCATACC TACATCCCTT TCTACGGCAT CCTGGGAGCC CTCCTTTTCC 360
 TCAACTTCAT CAGGTTTCCTG GAGAGCCACT GGTTCGTGTG GGTACACAG ATGAATCACA 420
 TCGTCATGGA GATTGACCAG GAGGCTACC GTGACTGGTT CAGTAGCCAG CTGACAGCCA 480
 20 CCTGCAACGT GGAGCAGTCC TTCTTCAACG ACTGGTTCAG TGGACACCTT AACTTCCAGA 540
 TTGAGCACCA CCTCTTCCCC ACCATGCCCC GGCACAACCT ACACAAGATC GCCCCGCTGG 600
 25 TGAAGTCTCT ATGTGCCAAG CATGGCATTG AATACCAGGA GAAGCCGCTA CTGAGGGCCC 660
 TGCTGGACAT CATCAGGTCC CTGAAGAAGT CTGGGAAGCT GTGGCTGGAC GCCTACCTTC 720
 30 ACAAATGAAG CCACAGCCCC CGGGACACCG TGGGGAAGGG GTGCAGGTGG GGTGATGGCC 780
 AGAGGAATGA TGGGCTTTTG TTCTGAGGGG TGTCCGAGAG GCTGGTGTAT GCACTGCTCA 840
 CGGACCCCAT GTTGGATCTT TCTCCCTTTC TCCTCTCCTT TTTCTCTTCA CATCTCCCCC 900
 35 ATAGCACCTT GCCCTCATGG GAQCTGCCCT CCCTCAGCCG TCAGCCATCA GCCATGGCCC 960
 TCCAGTGCC TCCTAGCCCC TTCTTCCAAG GAGCAGAGAG GTGGCCACCG GGGGTGGCTC 1020
 40 TGTCCTACCT CCACTCTCTG CCCCTAAAGA TGGGAGGAGA CCAGCGGTCC ATGGGTCTGG 1080
 CCTGTGAGTC TCCCCTTGCA GCCTGGTCAC TAGGCATCAC CCCCCTTTG GTTCTTCAGA 1140
 TGCTCTTGGG GTTCATAGGG GCAGGTCTTA GTCGGGCAGG GCCCCTGACC CTCCCGGCT 1200
 45 GGCTTCACTC TCCCTGACGG CTGCCATTGG TCCACCCTT CATAGAGAGG CCTGCTTTGT 1260
 TACAAAGCTC GGGTCTCCCT CCTGCAGCTC GGTAAAGTAC CCGAGGCCTC TCTTAAGATG 1320
 50 TCCAGGGCCC CAGGCCCGCG GGCACAGCCA GCCCAAACCT TGGGCCCTGG AAGAGTCCTC 1380
 CACCCCATCA CTAGAGTGCT CTGACCCTGG GCTTTCACGG GCCCCATTCC ACCGCCTCCC 1440
 CAACTTGAGC CTGTGACCTT GGGACCAAAG GGGGAGTCCC TCGTCTCTTG TGA CTGAGCA 1500
 55 GAGGCAGTGG CCACGTTTCAG GGAGGGGCCG GCTGGCCTGG AGGCTCAGCC CACCCTCCAG 1560
 CTTTTCCTCA GGGTGTCTTG AGGTCCAAGA TTCTGGAGCA ATCTGACCCT TCTCCAAAGG 1620
 60 CTCTGTTATC AGCTGGGCAG TGCCAGCCAA TCCCTGGCCA TTTGGCCCCA GGGGACGTGG 1680
 GCCCTG 1686

(2) INFORMATION FOR SEQ ID NO:32:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1843 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

5

(ii) MOLECULE TYPE: other nucleic acid (Contig 2535)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:32:

10

GTCTTTTACT TTGGCAATGG CTGGATTCCT ACCCTCATCA CGGCCTTTGT CCTTGCTACC 60

TCTCAGGCC AAGCTGGATG GCTGCAACAT GATTATGGCC ACCTGTCTGT CTACAGAAAA 120

15

CCCAAGTGA ACCACCTTGT CCACAAATTC GTCATTGGCC ACTTAAAGGG TGCCTCTGCC 180

AAGTGGTGA ATCATCGCCA CTTCCAGCAC CACGCCAAGC CTAACATCTT CCACAAGGAT 240

20

CCCGATGTGA ACATGCTGCA CGTGTTTGTT CTGGGCGAAT GGCAGCCCAT CGAGTACGGC 300

AAGAAGAAGC TGAAATACCT GCCCTACAAT CACCAGCACG AATACTTCTT CCTGATTGGG 360

CCGCCGCTGC TCATCCCCAT GTATTTCCAG TACCAGATCA TCATGACCAT GATCGTCCAT 420

25

AAGAACTGGG TGGACCTGGC CTGGGCCGTC AGCTACTACA TCCGGTCTT CATCACCTAC 480

ATCCCTTTCT ACGGCATCCT GGGAGCCCTC CTTTTCCTCA ACTTCATCAG GTTCTGGAG 540

30

AGCCACTGGT TTGTGTGGGT CACACAGATG AATCACATCG TCATGGAGAT TGACCAGGAG 600

GCCTACCGTG ACTGGTTCAG TAGCCAGCTG ACAGCCACCT GCAACGTGGA GCAGTCCTTC 660

TTCAACGACT GGTTCAGTGG ACACCTTAAC TTCCAGATTG AGCACCACCT CTTCCCCACC 720

35

ATGCCCCGGC ACAACTTACA CAAGATCGCC CCGCTGGTGA AGTCTCTATG TGCCAAGCAT 780

GGCATTGAAT ACCAGGAGAA GCCGCTACTG AGGGCCCTGC TGGACATCAT CAGGTCCCTG 840

40

AAGAAGTCTG GGAAGCTGTG GCTGGACGCC TACCTTCACA AATGAAGCCA CAGCCCCCGG 900

GACACCGTGG GGAAGGGGTG CAGGTGGGGT GATGGCCAGA GGAATGATGG GCTTTTGTTC 960

TGAGGGGTGT CCGAGAGGCT GGTGTATGCA CTGCTCACGG ACCCCATGTT GGATCTTTCT 1020

45

CCCTTTCTCC TCTCCTTTT CTCTTCACAT CTCCCCATA GCACCCTGCC CTCATGGGAC 1080

CTGCCCTCCC TCAGCCGTCA GCCATCAGCC ATGGCCCTCC CAGTGCCTCC TAGCCCTTC 1140

50

TTCCAAGGAG CAGAGAGGTG GCCACCGGG GTGGCTCTGT CCTACCTCCA CTCTCTGCCC 1200

CTAAAGATGG GAGGAGACCA GCGGTCCATG GGTCTGGCCT GTGAGTCTCC CTTGCAGCC 1260

TGGTCACTAG GCATACCCC CGCTTTGGTT CTTCAGATGC TCTTGGGGTT CATAGGGGCA 1320

55

GGTCTAGTC GGGCAGGGCC CCTGACCCTC CCGGCCTGGC TTCACTCTCC CTGACGGCTG 1380

CCATTGGTCC ACCCTTTCAT AGAGAGGCCT GCTTTGTAC AAAGCTCGGG TCTCCCTCCT 1440

60

GCAGCTCGGT TAAGTACCCG AGGCCTCTCT TAAGATGTCC AGGGCCCCAG GCCCGCGGGC 1500

ACAGCCAGCC CAAACCTTGG GCCCTGGAAG AGTCCTCCAC CCCATCACTA GAGTGCTCTG 1560

ACCCTGGGCT TTCACGGGCC CCATTCCACC GCCTCCCCAA CTTGAGCCTG TGACCTTGGG 1620

65

ACCAAAGGGG GAGTCCCTCG TCTCTGTGA CTCAGCAGAG GCAGTGGCCA CGTTCAGGGA 1680

GGGGCCGGCT GGCCTGGAGG CTCAGCCCAC CCTCCAGCTT TTCCTCAGGG TGTCTGAGG 1740
 TCCAAGATTC TGGAGCAATC TGACCCTTCT CCAAAGGCTC TGTATCAGC TGGGCAGTGC 1800
 5 CAGCCAATCC CTGGCCATTT GGCCCCAGGG GACGTGGGCC CTG 1843

(2) INFORMATION FOR SEQ ID NO:33:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 2257 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid (Edited Contig 253538a)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:33:

20 CAGGGACCTA CCCGCGCTA CTTACCTGG GACGAGGTGG CCCAGCGCTC AGGGTGCGAG 60
 GAGCGGTGGC TAGTGATCGA CCGTAAGGTG TACAACATCA GCGAGTTCAC CCGCCGGCAT 120
 25 CCAGGGGGCT CCCGGGTCAT CAGCCACTAC GCCGGGCAGG ATGCCACGGA TCCCTTTGTG 180
 GCCTTCCACA TCAACAAGGG CTTGTGAAG AAGTATATGA ACTCTCTCCT GATTGGAGAA 240
 CTGTCTCCAG AGCAGCCCAG CTTTGAGCCC ACCAAGAATA AAGAGCTGAC AGATGAGTTC 300
 30 CGGGAGCTGC GGGCCACAGT GGAGCGGATG GGGCTCATGA AGGCCAACCA TGTCTTCTTC 360
 CTGCTGTACC TGCTGCACAT CTTGCTGCTG GATGGTGCAG CCTGGCTCAC CCTTTGGGTC 420
 TTTGGGACGT CCTTTTTGCC CTTCTCTCTC TGTGCGGTGC TGCTCAGTGC AGTTCAGCAG 480
 35 GCCCAAGCTG GATGGCTGCA ACATGATTAT GGCCACCTGT CTGTCTACAG AAAACCCAAG 540
 TGGAACCACC TTGTCCACAA ATTCGTCATT GGCCACTTAA AGGGTGCCTC TGCCAACTGG 600
 40 TGGAATCATC GCCACTTCCA GCACCACGCC AAGCCTAACA TCTTCCACAA GGATCCCGAT 660
 GTGAACATGC TGCACGTGTT TGTCTGGGC GAATGGCAGC CCATCGAGTA CGGCAAGAAG 720
 AAGCTGAAAT ACCTGCCCTA CAATCACCAG CACGAATACT TCTTCCTGAT TGGGCCGCGC 780
 45 CTGCTCATCC CCATGTATTT CCAGTACCAG ATCATCATGA CCATGATCGT CCATAAGAAC 840
 TGGGTGGACC TGGCCTGGGC CGTCAGCTAC TACATCCGGT TCTTCATCAC CTACATCCCT 900
 50 TTCTACGGCA TCCTGGGAGC CCTCCTTTTC CTCAACTTCA TCAGGTTCCCT GGAGAGCCAC 960
 TGGTTTGTGT GGGTCACACA GATGAATCAC ATCGTCATGG AGATTGACCA GGAGGCCTAC 1020
 55 CGTGACTGGT TCAGTAGCCA GCTGACAGCC ACCTGCAACG TGGAGCAGTC CTTCTTCAAC 1080
 GACTGGTTCA GTGGACACCT TAACTTCCAG ATTGAGCACC ACCTCTTCCC CACCATGCCC 1140
 CGGCACAAC TACACAAGAT CGCCCCGCTG GTGAAGTCTC TATGTGCCAA GCATGGCATT 1200
 60 GAATACCAGG AGAAGCCGCT ACTGAGGGCC CTGCTGGACA TCATCAGGTC CCTGAAGAAG 1260
 TCTGGGAAGC TGTGGCTGGA CGCCTACCTT CACAAATGAA GCCACAGCCC CCGGGACACC 1320
 65 GTGGGAAGG GGTGCAGGTG GGGTGATGGC CAGAGGAATG ATGGGCTTTT GTTCTGAGGG 1380
 GTGTCCGAGA GGCTGGTGTG TGCACGTCTC ACGGACCCCA TGTGGATCTT TTCTCCCTTT 1440

CTCCTCTCCT TTTTCTCTTC ACATCTCCCC CATAGCACCC TGCCCTCATG GGACCTGCCC 1500
 5 TCCCTCAGCC GTCAGCCATC AGCCATGGCC CTCCCAGTGC CTCCTAGCCC CTTCTTCCAA 1560
 GGAGCAGAGA GGTGGCCACC GGGGGTGGCT CTGTCTTACC TCCACTCTCT GCCCCTAAAG 1620
 ATGGGAGGAG ACCAGCGGTC CATGGGTCTG GCCTGTGAGT CTCCCCTTGC AGCCTGGTCA 1680
 10 CTAGGCATCA CCCCCGCTTT GGTCTTCAG ATGCTCTTGG GGTTCATAGG GGCAGGTCCT 1740
 AGTCGGGCAG GGCCCCGTGAC CCTCCCGGCC TGGCTTCACT CTCCCTGACG GCTGCCATTG 1800
 15 GTCCACCCTT TCATAGAGAG GCCTGCTTTG TTACAAAGCT CGGGTCTCCC TCCTGCAGCT 1860
 CGGTAAAGTA CCGAGGCCT CTCTTAAGAT GTCCAGGGCC CCAGGCCCGC GGGCACAGCC 1920
 AGCCCAAACC TTGGGCCCTG GAAGAGTCCT CCACCCCATC ACTAGAGTGC TCTGACCCTG 1980
 20 GGCTTTCACG GGCCCCATTC CACCGCCTCC CCAACTTGAG CCTGTGACCT TGGGACCAAA 2040
 GGGGGAGTCC CTCGTCTCTT GTGACTCAGC AGAGGCAGTG GCCACGTTCA GGGAGGGGCC 2100
 25 GGCTGGCCTG GAGGCTCAGC CCACCCTCCA GCTTTTCCTC AGGGTGTCTT GAGGTCCAAG 2160
 ATTCTGGAGC AATCTGACCC TTCTCAAAG GCTCTGTAT CAGCTGGGCA GTGCCAGCCA 2220
 ATCCCTGGCC ATTTGGCCCC AGGGGACGTG GGCCCTG 2257

(2) INFORMATION FOR SEQ ID NO:34:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 411 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: amino acid (Translation of Contig 2692004)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:34:

His Ala Asp Arg Arg Arg Glu Ile Leu Ala Lys Tyr Pro Glu Ile
 1 5 10 15
 Lys Ser Leu Met Lys Pro Asp Pro Asn Leu Ile Trp Ile Ile Ile
 20 25 30
 Met Met Val Leu Thr Gln Leu Gly Ala Phe Tyr Ile Val Lys Asp
 35 40 45
 50 Leu Asp Trp Lys Trp Val Ile Phe Gly Ala Tyr Ala Phe Gly Ser
 50 55 60
 Cys Ile Asn His Ser Met Thr Leu Ala Ile His Glu Ile Ala His
 65 70 75
 55 Asn Ala Ala Phe Gly Asn Cys Lys Ala Met Trp Asn Arg Trp Phe
 80 85 90
 Gly Met Phe Ala Asn Leu Pro Ile Gly Ile Pro Tyr Ser Ile Ser
 95 100 105
 Phe Lys Arg Tyr His Met Asp His His Arg Tyr Leu Gly Ala Asp
 110 115 120
 60 Gly Val Asp Val Asp Ile Pro Thr Asp Phe Glu Gly Trp Phe Phe
 125 130 135
 Cys Thr Ala Phe Arg Lys Phe Ile Trp Val Ile Leu Gln Pro Leu
 140 145 150
 65 Phe Tyr Ala Phe Arg Pro Leu Phe Ile Asn Pro Lys Pro Ile Thr
 155 160 165
 Tyr Leu Glu Val Ile Asn Thr Val Ala Gln Val Thr Phe Asp Ile

170 175 180
 Leu Ile Tyr Tyr Phe Leu Gly Ile Lys Ser Leu Val Tyr Met Leu
 185 190 195
 5 Ala Ala Ser Leu Leu Gly Leu Gly Leu His Pro Ile Ser Gly His
 200 205 210
 Phe Ile Ala Glu His Tyr Met Phe Leu Lys Gly His Glu Thr Tyr
 215 220 225
 Ser Tyr Tyr Gly Pro Leu Asn Leu Leu Thr Phe Asn Val Gly Tyr
 230 235 240
 10 His Asn Glu His His Asp Phe Pro Asn Ile Pro Gly Lys Ser Leu
 245 250 255
 Pro Leu Val Arg Lys Ile Ala Ala Glu Tyr Tyr Asp Asn Leu Pro
 260 265 270
 15 His Tyr Asn Ser Trp Ile Lys Val Leu Tyr Asp Phe Val Met Asp
 275 280 285
 Asp Thr Ile Ser Pro Tyr Ser Arg Met Lys Arg His Gln Lys Gly
 290 295 300
 Glu Met Val Leu Glu *** Ile Ser Leu Val Pro Lys Gly Phe Phe
 305 310 315
 20 Ser Lys Thr Leu Asp Asp Lys Met Glu Phe Leu His Tyr *** Thr
 320 325 330
 *** Asp Gln *** Cys Ser Glu Ala Pro Leu Ala Gln Phe Gln Ser
 335 340 345
 25 Lys Ser Ser Val Ile Pro Arg Ser Glu Ser Gly Phe *** Thr Val
 350 355 360
 Ser Leu Thr Leu Tyr Cys Ser Val Ser Leu Thr Gly Asn Leu ***
 365 370 375
 Leu Val Tyr Tyr Arg His *** Gly Cys Phe Thr His Val Cys His
 380 385 390
 30 Phe Ile Ser Ile Ser Phe Lys Lys Leu Leu Lys Ser Tyr Phe Ala
 400 405 410
 Arg

(2) INFORMATION FOR SEQ ID NO:35:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 218 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: amino acid (Translation of Contig 2153526)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:35:

Tyr Leu Leu Arg Pro Leu Leu Pro His Leu Cys Ala Thr Ile Gly
 1 5 10 15
 50 Ala Glu Ser Phe Leu Gly Leu Phe Phe Ile Val Arg Phe Leu Glu
 20 25 30
 Ser Asn Trp Phe Val Trp Val Thr Gln Met Asn His Ile Pro Met
 35 40 45
 His Ile Asp His Asp Arg Asn Met Asp Trp Val Ser Thr Gln Leu
 50 55 60
 55 Gln Ala Thr Cys Asn Val His Lys Ser Ala Phe Asn Asp Trp Phe
 65 70 75
 Ser Gly His Leu Asn Phe Gln Ile Glu His His Leu Phe Pro Thr
 80 85 90
 60 Met Pro Arg His Asn Tyr His Lys Val Ala Pro Leu Val Gln Ser
 95 100 105
 Leu Cys Ala Lys His Gly Ile Glu Tyr Gln Ser Lys Pro Leu Leu
 110 115 120
 Ser Ala Phe Ala Asp Ile Ile His Ser Leu Lys Glu Ser Gly Gln
 125 130 135
 65 Leu Trp Leu Asp Ala Tyr Leu His Gln *** Gln Gln Pro Pro Cys
 140 145 150

Pro Val Trp Lys Lys Arg Arg Lys Thr Leu Glu Pro Arg Gln Arg
 155 160 165
 Gly Ala *** Gly Thr Met Pro Leu *** Phe Asn Thr Gln Arg Gly
 170 175 180
 5 Leu Gly Leu Gly Thr *** Ser Leu *** Leu Lys Leu Leu Pro Phe
 185 190 195
 Ile Phe *** Pro Gln Phe *** Asp Pro Lys Trp Gly Val Asp Thr
 200 205 210
 10 Glu Val Pro Arg Arg Glu Gly Ala
 215

(2) INFORMATION FOR SEQ ID NO:36:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 86 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: amino acid (Translation of Contig 3506132)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:36:

Val Phe Tyr Phe Gly Asn Gly Trp Ile Pro Thr Leu Ile Thr Ala
 1 5 10 15
 30 Phe Val Leu Ala Thr Ser Gln Ala Gln Ala Gly Trp Leu Gln His
 20 25 30
 Asp Tyr Gly His Leu Ser Val Tyr Arg Lys Pro Lys Trp Asn His
 35 40 45
 35 Leu Val His Lys Phe Val Ile Gly His Leu Lys Gly Ala Ser Ala
 50 55 60
 Asn Trp Trp Asn His Arg His Phe Gln His His Ala Lys Pro Asn
 65 70 75
 40 Leu Gly Glu Trp Gln Pro Ile Glu Tyr Gly Lys Xxx
 80 85

(2) INFORMATION FOR SEQ ID NO:37:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 306 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: amino acid (Translation of Contig 3854933)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:37:

Gln Gly Pro Thr Pro Arg Tyr Phe Thr Trp Asp Glu Val Ala Gln
 1 5 10 15
 Arg Ser Gly Cys Glu Glu Arg Trp Leu Val Ile Asp Arg Lys Val
 20 25 30
 60 Tyr Asn Ile Ser Glu Phe Thr Arg Arg His Pro Gly Gly Ser Arg
 35 40 45
 Val Ile Ser His Tyr Ala Gly Gln Asp Ala Thr Asp Pro Phe Val
 50 55 60
 Ala Phe His Ile Asn Lys Gly Leu Val Lys Lys Tyr Met Asn Ser
 65 70 75
 Leu Leu Ile Gly Glu Leu Ser Pro Glu Gln Pro Ser Phe Glu Pro

		80		85		90									
	Thr	Lys	Asn	Lys	Glu	Leu	Thr	Asp	Glu	Phe	Arg	Glu	Leu	Arg	Ala
				95		100									105
5	Thr	Val	Glu	Arg	Met	Gly	Leu	Met	Lys	Ala	Asn	His	Val	Phe	Phe
				110		115									120
	Leu	Leu	Tyr	Leu	Leu	His	Ile	Leu	Leu	Leu	Asp	Gly	Ala	Ala	Trp
				125		130									135
	Leu	Thr	Leu	Trp	Val	Phe	Gly	Thr	Ser	Phe	Leu	Pro	Phe	Leu	Leu
				140		145									150
10	Cys	Ala	Val	Leu	Leu	Ser	Ala	Val	Gln	Ala	Gln	Ala	Gly	Trp	Leu
				155		160									165
	Gln	His	Asp	Phe	Gly	His	Leu	Ser	Val	Phe	Ser	Thr	Ser	Lys	Trp
				170		175									180
15	Asn	His	Leu	Leu	His	His	Phe	Val	Ile	Gly	His	Leu	Lys	Gly	Ala
				185		190									195
	Pro	Ala	Ser	Trp	Trp	Asn	His	Met	His	Phe	Gln	His	His	Ala	Lys
				200		205									210
	Pro	Asn	Cys	Phe	Arg	Lys	Asp	Pro	Asp	Ile	Asn	Met	His	Pro	Phe
				215		220									225
20	Phe	Phe	Ala	Leu	Gly	Lys	Ile	Leu	Ser	Val	Glu	Leu	Gly	Lys	Gln
				230		235									240
	Lys	Lys	Lys	Tyr	Met	Pro	Tyr	Asn	His	Gln	His	Xxx	Tyr	Phe	Phe
				245		250									255
25	Leu	Ile	Gly	Pro	Pro	Ala	Leu	Leu	Pro	Leu	Tyr	Phe	Gln	Trp	Tyr
				260		265									270
	Ile	Phe	Tyr	Phe	Val	Ile	Gln	Arg	Lys	Lys	Trp	Val	Asp	Leu	Ala
				275		280									285
	Trp	Ile	Ser	Lys	Gln	Glu	Tyr	Asp	Glu	Ala	Gly	Leu	Pro	Leu	Ser
				290		295									300
30	Thr	Ala	Asn	Ala	Ser	Lys									
				305											

(2) INFORMATION FOR SEQ ID NO:38:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 566 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: amino acid (Translation of Contig 2511785)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:38:

	His	Leu	Lys	Gly	Ala	Ser	Ala	Asn	Trp	Trp	Asn	His	Arg	His	Phe
	1				5					10					15
50	Gln	His	His	Ala	Lys	Pro	Asn	Ile	Phe	His	Lys	Asp	Pro	Asp	Val
				20						25					30
	Asn	Met	Leu	His	Val	Phe	Val	Leu	Gly	Glu	Trp	Gln	Pro	Ile	Glu
				35						40					45
	Tyr	Gly	Lys	Lys	Lys	Leu	Lys	Tyr	Leu	Pro	Tyr	Asn	His	Gln	His
				50						55					60
55	Glu	Tyr	Phe	Phe	Leu	Ile	Gly	Pro	Pro	Leu	Leu	Ile	Pro	Met	Tyr
				65						70					75
	Phe	Gln	Tyr	Gln	Ile	Ile	Met	Thr	Met	Ile	Val	His	Lys	Asn	Trp
				80						85					90
	Val	Asp	Leu	Ala	Trp	Ala	Val	Ser	Tyr	Tyr	Ile	Arg	Phe	Phe	Ile
				95						100					105
60	Thr	Tyr	Ile	Pro	Phe	Tyr	Gly	Ile	Leu	Gly	Ala	Leu	Leu	Phe	Leu
				110						115					120
	Asn	Phe	Ile	Arg	Phe	Leu	Glu	Ser	His	Trp	Phe	Val	Trp	Val	Thr
				125						130					135
65	Gln	Met	Asn	His	Ile	Val	Met	Glu	Ile	Asp	Gln	Glu	Ala	Tyr	Arg
				140						145					150

Asp Trp Phe Ser Ser Gln Leu Thr Ala Thr Cys Asn Val Glu Gln
 155 160 165
 Ser Phe Phe Asn Asp Trp Phe Ser Gly His Leu Asn Phe Gln Ile
 170 175 180
 5 Glu His His Leu Phe Pro Thr Met Pro Arg His Asn Leu His Lys
 185 190 195
 Ile Ala Pro Leu Val Lys Ser Leu Cys Ala Lys His Gly Ile Glu
 200 205 210
 10 Tyr Gln Glu Lys Pro Leu Leu Arg Ala Leu Leu Asp Ile Ile Arg
 215 220 225
 Ser Leu Lys Lys Ser Gly Lys Leu Trp Leu Asp Ala Tyr Leu His
 230 235 240
 Lys *** Ser His Ser Pro Arg Asp Thr Val Gly Lys Gly Cys Arg
 245 250 255
 15 Trp Gly Asp Gly Gln Arg Asn Asp Gly Leu Leu Phe *** Gly Val
 260 265 270
 Ser Glu Arg Leu Val Tyr Ala Leu Leu Thr Asp Pro Met Leu Asp
 275 280 285
 20 Leu Ser Pro Phe Leu Leu Ser Phe Phe Ser Ser His Leu Pro His
 290 295 300
 Ser Thr Leu Pro Ser Trp Asp Leu Pro Ser Leu Ser Arg Gln Pro
 305 310 315
 Ser Ala Met Ala Leu Pro Val Pro Pro Ser Pro Phe Phe Gln Gly
 320 325 330
 25 Ala Glu Arg Trp Pro Pro Gly Val Ala Leu Ser Tyr Leu His Ser
 335 340 345
 Leu Pro Leu Lys Met Gly Gly Asp Gln Arg Ser Met Gly Leu Ala
 350 355 360
 30 Cys Glu Ser Pro Leu Ala Ala Trp Ser Leu Gly Ile Thr Pro Ala
 365 370 375
 Leu Val Leu Gln Met Leu Leu Gly Phe Ile Gly Ala Gly Pro Ser
 380 385 390
 Arg Ala Gly Pro Leu Thr Leu Pro Ala Trp Leu His Ser Pro ***
 400 405 410
 35 Arg Leu Pro Leu Val His Pro Phe Ile Glu Arg Pro Ala Leu Leu
 415 420 425
 Gln Ser Ser Gly Leu Pro Pro Ala Ala Arg Leu Ser Thr Arg Gly
 430 435 440
 40 Leu Ser *** Asp Val Gln Gly Pro Arg Pro Ala Gly Thr Ala Ser
 445 450 455
 Pro Asn Leu Gly Pro Trp Lys Ser Pro Pro Pro His His *** Ser
 460 465 470
 Ala Leu Thr Leu Gly Phe His Gly Pro His Ser Thr Ala Ser Pro
 475 480 485
 45 Thr *** Ala Cys Asp Leu Gly Thr Lys Gly Gly Val Pro Arg Leu
 490 495 500
 Leu *** Leu Ser Arg Gly Ser Gly His Val Gln Gly Gly Ala Gly
 505 510 515
 50 Trp Pro Gly Gly Ser Ala His Pro Pro Ala Phe Pro Gln Gly Val
 520 525 530
 Leu Arg Ser Lys Ile Leu Glu Gln Ser Asp Pro Ser Pro Lys Ala
 535 540 545
 Leu Leu Ser Ala Gly Gln Cys Gln Pro Ile Pro Gly His Leu Ala
 550 555 560
 55 Pro Gly Asp Val Gly Pro Xxx
 565

(2) INFORMATION FOR SEQ ID NO:39:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 619 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: amino acid (Translation of Contig 2535)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:39:

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Val	Phe	Tyr	Phe	Gly	Asn	Gly	Trp	Ile	Pro	Thr	Leu	Ile	Thr	Ala	
1				5					10					15	
Phe	Val	Leu	Ala	Thr	Ser	Gln	Ala	Gln	Ala	Gly	Trp	Leu	Gln	His	
				20					25					30	
Asp	Tyr	Gly	His	Leu	Ser	Val	Tyr	Arg	Lys	Pro	Lys	Trp	Asn	His	
				35					40					45	
Leu	Val	His	Lys	Phe	Val	Ile	Gly	His	Leu	Lys	Gly	Ala	Ser	Ala	
				50					55					60	
Asn	Trp	Trp	Asn	His	Arg	His	Phe	Gln	His	His	Ala	Lys	Pro	Asn	
				65					70					75	
Ile	Phe	His	Lys	Asp	Pro	Asp	Val	Asn	Met	Leu	His	Val	Phe	Val	
				80					85					90	
Leu	Gly	Glu	Trp	Gln	Pro	Ile	Glu	Tyr	Gly	Lys	Lys	Lys	Leu	Lys	
				95					100					105	
Tyr	Leu	Pro	Tyr	Asn	His	Gln	His	Glu	Tyr	Phe	Phe	Leu	Ile	Gly	
				110					115					120	
Pro	Pro	Leu	Leu	Ile	Pro	Met	Tyr	Phe	Gln	Tyr	Gln	Ile	Ile	Met	
				125					130					135	
Thr	Met	Ile	Val	His	Lys	Asn	Trp	Val	Asp	Leu	Ala	Trp	Ala	Val	
				140					145					150	
Ser	Tyr	Tyr	Ile	Arg	Phe	Phe	Ile	Thr	Tyr	Ile	Pro	Phe	Tyr	Gly	
				155					160					165	
Ile	Leu	Gly	Ala	Leu	Leu	Phe	Leu	Asn	Phe	Ile	Arg	Phe	Leu	Glu	
				170					175					180	
Ser	His	Trp	Phe	Val	Trp	Val	Thr	Gln	Met	Asn	His	Ile	Val	Met	
				185					190					195	
Glu	Ile	Asp	Gln	Glu	Ala	Tyr	Arg	Asp	Trp	Phe	Ser	Ser	Gln	Leu	
				200					205					210	
Thr	Ala	Thr	Cys	Asn	Val	Glu	Gln	Ser	Phe	Phe	Asn	Asp	Trp	Phe	
				215					220					225	
Ser	Gly	His	Leu	Asn	Phe	Gln	Ile	Glu	His	His	Leu	Phe	Pro	Thr	
				230					235					240	
Met	Pro	Arg	His	Asn	Leu	His	Lys	Ile	Ala	Pro	Leu	Val	Lys	Ser	
				245					250					255	
Leu	Cys	Ala	Lys	His	Gly	Ile	Glu	Tyr	Gln	Glu	Lys	Pro	Leu	Leu	
				260					265					270	
Arg	Ala	Leu	Leu	Asp	Ile	Ile	Arg	Ser	Leu	Lys	Lys	Ser	Gly	Lys	
				275					280					285	
Leu	Trp	Leu	Asp	Ala	Tyr	Leu	His	Lys	***	Ser	His	Ser	Pro	Arg	
				290					295					300	
Asp	Thr	Val	Gly	Lys	Gly	Cys	Arg	Trp	Gly	Asp	Gly	Gln	Arg	Asn	
				305					310					315	
Asp	Gly	Leu	Leu	Phe	***	Gly	Val	Ser	Glu	Arg	Leu	Val	Tyr	Ala	
				320					325					330	
Leu	Leu	Thr	Asp	Pro	Met	Leu	Asp	Leu	Ser	Pro	Phe	Leu	Leu	Ser	
				335					340					345	
Phe	Phe	Ser	Ser	His	Leu	Pro	His	Ser	Thr	Leu	Pro	Ser	Trp	Asp	
				350					355					360	
Leu	Pro	Ser	Leu	Ser	Arg	Gln	Pro	Ser	Ala	Met	Ala	Leu	Pro	Val	
				365					370					375	
Pro	Pro	Ser	Pro	Phe	Phe	Gln	Gly	Ala	Glu	Arg	Trp	Pro	Pro	Gly	
				380					385					390	
Val	Ala	Leu	Ser	Tyr	Leu	His	Ser	Leu	Pro	Leu	Lys	Met	Gly	Gly	
				400					405					410	
Asp	Gln	Arg	Ser	Met	Gly	Leu	Ala	Cys	Glu	Ser	Pro	Leu	Ala	Ala	
				415					420					425	
Trp	Ser	Leu	Gly	Ile	Thr	Pro	Ala	Leu	Val	Leu	Gln	Met	Leu	Leu	
				430					435					440	
Gly	Phe	Ile	Gly	Ala	Gly	Pro	Ser	Arg	Ala	Gly	Pro	Leu	Thr	Leu	
				445					450					455	

Pro Ala Trp Leu His Ser Pro *** Arg Leu Pro Leu Val His Pro
 460 465 470
 Phe Ile Glu Arg Pro Ala Leu Leu Gln Ser Ser Gly Leu Pro Pro
 475 480 485
 5 Ala Ala Arg Leu Ser Thr Arg Gly Leu Ser *** Asp Val Gln Gly
 490 495 500
 Pro Arg Pro Ala Gly Thr Ala Ser Pro Asn Leu Gly Pro Trp Lys
 505 510 515
 10 Ser Pro Pro Pro His His *** Ser Ala Leu Thr Leu Gly Phe His
 520 525 530
 Gly Pro His Ser Thr Ala Ser Pro Thr *** Ala Cys Asp Leu Gly
 535 540 545
 Thr Lys Gly Gly Val Pro Arg Leu Leu *** Leu Ser Arg Gly Ser
 550 555 560
 15 Gly His Val Gln Gly Gly Ala Gly Trp Pro Gly Gly Ser Ala His
 565 570 575
 Pro Pro Ala Phe Pro Gln Gly Val Leu Arg Ser Lys Ile Leu Glu
 580 585 590
 20 Gln Ser Asp Pro Ser Pro Lys Ala Leu Leu Ser Ala Gly Gln Cys
 595 600 605
 Gln Pro Ile Pro Gly His Leu Ala Pro Gly Asp Val Gly Pro Xxx
 610 615 620

(2) INFORMATION FOR SEQ ID NO:40:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 757 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: amino acid (Translation of Contig 253538a)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:40:

Gln Gly Pro Thr Pro Arg Tyr Phe Thr Trp Asp Glu Val Ala Gln
 1 5 10 15
 Arg Ser Gly Cys Glu Glu Arg Trp Leu Val Ile Asp Arg Lys Val
 20 25 30
 Tyr Asn Ile Ser Glu Phe Thr Arg Arg His Pro Gly Gly Ser Arg
 35 40 45
 45 Val Ile Ser His Tyr Ala Gly Gln Asp Ala Thr Asp Pro Phe Val
 50 55 60
 Ala Phe His Ile Asn Lys Gly Leu Val Lys Lys Tyr Met Asn Ser
 65 70 75
 50 Leu Leu Ile Gly Glu Leu Ser Pro Glu Gln Pro Ser Phe Glu Pro
 80 85 90
 Thr Lys Asn Lys Glu Leu Thr Asp Glu Phe Arg Glu Leu Arg Ala
 95 100 105
 Thr Val Glu Arg Met Gly Leu Met Lys Ala Asn His Val Phe Phe
 110 115 120
 55 Leu Leu Tyr Leu Leu His Ile Leu Leu Leu Asp Gly Ala Ala Trp
 125 130 135
 Leu Thr Leu Trp Val Phe Gly Thr Ser Phe Leu Pro Phe Leu Leu
 140 145 150
 60 Cys Ala Val Leu Leu Ser Ala Val Gln Gln Ala Gln Ala Gly Trp
 155 160 165
 Leu Gln His Asp Tyr Gly His Leu Ser Val Tyr Arg Lys Pro Lys
 170 175 180
 Trp Asn His Leu Val His Lys Phe Val Ile Gly His Leu Lys Gly
 185 190 195
 65 Ala Ser Ala Asn Trp Trp Asn His Arg His Phe Gln His His Ala
 200 205 210

	Lys	Pro	Asn	Ile	Phe	His	Lys	Asp	Pro	Asp	Val	Asn	Met	Leu	His	215	220	225
	Val	Phe	Val	Leu	Gly	Glu	Trp	Gln	Pro	Ile	Glu	Tyr	Gly	Lys	Lys	230	235	240
5	Lys	Leu	Lys	Tyr	Leu	Pro	Tyr	Asn	His	Gln	His	Glu	Tyr	Phe	Phe	245	250	255
	Leu	Ile	Gly	Pro	Pro	Leu	Leu	Ile	Pro	Met	Tyr	Phe	Gln	Tyr	Gln	260	265	270
10	Ile	Ile	Met	Thr	Met	Ile	Val	His	Lys	Asn	Trp	Val	Asp	Leu	Ala	275	280	285
	Trp	Ala	Val	Ser	Tyr	Tyr	Ile	Arg	Phe	Phe	Ile	Thr	Tyr	Ile	Pro	290	295	300
	Phe	Tyr	Gly	Ile	Leu	Gly	Ala	Leu	Leu	Phe	Leu	Asn	Phe	Ile	Arg	305	310	315
15	Phe	Leu	Glu	Ser	His	Trp	Phe	Val	Trp	Val	Thr	Gln	Met	Asn	His	320	325	330
	Ile	Val	Met	Glu	Ile	Asp	Gln	Glu	Ala	Tyr	Arg	Asp	Trp	Phe	Ser	335	340	345
20	Ser	Gln	Leu	Thr	Ala	Thr	Cys	Asn	Val	Glu	Gln	Ser	Phe	Phe	Asn	350	355	360
	Asp	Trp	Phe	Ser	Gly	His	Leu	Asn	Phe	Gln	Ile	Glu	His	His	Leu	365	370	375
	Phe	Pro	Thr	Met	Pro	Arg	His	Asn	Leu	His	Lys	Ile	Ala	Pro	Leu	380	385	390
25	Val	Lys	Ser	Leu	Cys	Ala	Lys	His	Gly	Ile	Glu	Tyr	Gln	Glu	Lys	400	405	410
	Pro	Leu	Leu	Arg	Ala	Leu	Leu	Asp	Ile	Ile	Arg	Ser	Leu	Lys	Lys	415	420	425
30	Ser	Gly	Lys	Leu	Trp	Leu	Asp	Ala	Tyr	Leu	His	Lys	***	Ser	His	430	435	440
	Ser	Pro	Arg	Asp	Thr	Val	Gly	Lys	Gly	Cys	Arg	Trp	Gly	Asp	Gly	445	450	455
	Gln	Arg	Asn	Asp	Gly	Leu	Leu	Phe	***	Gly	Val	Ser	Glu	Arg	Leu	460	465	470
35	Val	Tyr	Ala	Leu	Leu	Thr	Asp	Pro	Met	Leu	Asp	Leu	Ser	Pro	Phe	475	480	485
	Leu	Leu	Ser	Phe	Phe	Ser	Ser	His	Leu	Pro	His	Ser	Thr	Leu	Pro	490	495	500
40	Ser	Trp	Asp	Leu	Pro	Ser	Leu	Ser	Arg	Gln	Pro	Ser	Ala	Met	Ala	505	510	515
	Leu	Pro	Val	Pro	Pro	Ser	Pro	Phe	Phe	Gln	Gly	Ala	Glu	Arg	Trp	520	525	530
	Pro	Pro	Gly	Val	Ala	Leu	Ser	Tyr	Leu	His	Ser	Leu	Pro	Leu	Lys	535	540	545
45	Met	Gly	Gly	Asp	Gln	Arg	Ser	Met	Gly	Leu	Ala	Cys	Glu	Ser	Pro	550	555	560
	Leu	Ala	Ala	Trp	Ser	Leu	Gly	Ile	Thr	Pro	Ala	Leu	Val	Leu	Gln	565	570	575
50	Met	Leu	Leu	Gly	Phe	Ile	Gly	Ala	Gly	Pro	Ser	Arg	Ala	Gly	Pro	580	585	590
	Leu	Thr	Leu	Pro	Ala	Trp	Leu	His	Ser	Pro	***	Arg	Leu	Pro	Leu	595	600	605
	Val	His	Pro	Phe	Ile	Glu	Arg	Pro	Ala	Leu	Leu	Gln	Ser	Ser	Gly	610	615	620
55	Leu	Pro	Pro	Ala	Ala	Arg	Leu	Ser	Thr	Arg	Gly	Leu	Ser	***	Asp	625	630	635
	Val	Gln	Gly	Pro	Arg	Pro	Ala	Gly	Thr	Ala	Ser	Pro	Asn	Leu	Gly	640	645	650
60	Pro	Trp	Lys	Ser	Pro	Pro	Pro	His	His	***	Ser	Ala	Leu	Thr	Leu	655	660	665
	Gly	Phe	His	Gly	Pro	His	Ser	Thr	Ala	Ser	Pro	Thr	***	Ala	Cys	670	675	680
	Asp	Leu	Gly	Thr	Lys	Gly	Gly	Val	Pro	Arg	Leu	Leu	***	Leu	Ser	685	690	695
65	Arg	Gly	Ser	Gly	His	Val	Gln	Gly	Gly	Ala	Gly	Trp	Pro	Gly	Gly	700	705	710

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Ser	Ala	His	Pro	Pro	Ala	Phe	Pro	Gln	Gly	Val	Leu	Arg	Ser	Lys
				715					720					725
Ile	Leu	Glu	Gln	Ser	Asp	Pro	Ser	Pro	Lys	Ala	Leu	Leu	Ser	Ala
				730					735					740
Gly	Gln	Cys	Gln	Pro	Ile	Pro	Gly	His	Leu	Ala	Pro	Gly	Asp	Val
				745					750					755
Gly	Pro	Xxx												

What is claimed is:

1. An isolated nucleic acid comprising:

a nucleotide sequence depicted in SEQ ID NO: 1 or SEQ ID NO: 3.

2. A polypeptide encoded by a nucleotide sequence according to claim 1.

3. A purified or isolated polypeptide comprising an amino acid sequence depicted in SEQ ID NO: 2 or SEQ ID NO: 4.

4. An isolated nucleic acid encoding a polypeptide having an amino acid sequence depicted in SEQ ID NO: 2 or SEQ ID NO: 4.

5. An isolated nucleic acid comprising a nucleotide sequence which encodes a polypeptide which desaturates a fatty acid molecule at carbon 6 or 12 from the carboxyl end of said polypeptide, wherein said nucleotide sequence has an average A/T content of less than about 60%.

6. The isolated nucleic acid according to Claim 5, wherein said nucleic acid is derived from a fungus.

7. The isolated nucleic acid according to Claim 6, wherein said fungus is of the genus *Mortierella*.

8. The isolated nucleic acid according to Claim 7, wherein said fungus is of the species *Mortierella alpina*.

9. An isolated nucleic acid, wherein the nucleotide sequence of said nucleic acid is depicted in SEQ ID NO: 1. or SEQ ID NO: 3.

10. An isolated or purified polypeptide which desaturates a fatty acid molecule at carbon 6 or 12 from the carboxyl end of said polypeptide, wherein said polypeptide is a eukaryotic polypeptide or is derived from a eukaryotic polypeptide.

11. The isolated or purified eukaryotic polypeptide according to Claim 10, wherein said eukaryotic polypeptide is derived from a fungus.

12. A nucleic acid comprising:

a fungal nucleotide sequence which is substantially identical to a sequence of at least 50 nucleotides in SEQ ID NO: 1 or SEQ ID NO: 3 or is complementary to a sequence of at least 50 nucleotides in SEQ ID NO: 1 or SEQ ID NO: 3.

13. An isolated nucleic acid having a nucleotide sequence with at least about 50% homology to SEQ ID NO: 1 or SEQ ID NO: 3.

14. An isolated nucleic acid having a nucleotide sequence with at least about 50% homology to sequence encoding an amino acid sequence depicted in SEQ ID NO: 2 or SEQ ID NO: 4.

15. The nucleic acid of claim 14, wherein said amino acid sequence depicted in SEQ ID NO: 2 is selected from the group consisting of amino acid residues 50-53, 39-43, 172-176, 204-213, and 390-402.

16. A nucleic acid construct comprising:

a nucleotide sequence depicted in a SEQ ID NO: 1 or SEQ ID NO: 3 linked to a heterologous nucleic acid.

17. A nucleic acid construct comprising:

5 a nucleotide sequence depicted in a SEQ ID NO: 1 or SEQ ID NO: 3 operably associated with an expression control sequence functional in a microbial cell.

10 18. The nucleic acid construct according to Claim 17, wherein said microbial cell is a yeast cell.

19. The nucleic acid construct according to Claim 17, wherein said nucleotide sequence is derived from a fungus.

15 20. The nucleic acid construct according to Claim 19, wherein said fungus is of the genus *Mortierella*.

21. The nucleic acid construct according to Claim 20, wherein said fungus is of the species *Mortierella alpina*.

20 22. A nucleic acid construct comprising:

25 a fungal nucleotide sequence which encodes a polypeptide comprising an amino acid sequence which corresponds to or is complementary to an amino acid sequence depicted in SEQ ID NO: 2 or SEQ ID NO: 4, wherein said nucleic acid is operably associated with an expression control sequence functional in a microbial cell, wherein said nucleotide sequence encodes a functionally active polypeptide which desaturates a fatty acid molecule at carbon 6 or 12 from the carboxyl end of a fatty acid molecule.

23. A nucleic acid construct comprising:

a nucleotide sequence having an A/T content of less than about 60% which encodes a functionally active $\Delta 6$ -desaturase having an amino acid sequence which corresponds to or is complementary to all of or a portion of an amino acid sequence depicted in a SEQ ID NO: 2, wherein said nucleotide sequence is operably associated with a transcription control sequence functional in a yeast cell.

24. A nucleic acid construct comprising:

a fungal nucleotide sequence which encodes a functionally active $\Delta 12$ -desaturase having an amino acid sequence which corresponds to or is complementary to all of or a portion of an amino acid sequence depicted in a SEQ ID NO: 4, wherein said nucleotide sequence is operably associated with a transcription control sequence functional in a yeast cell.

25. A recombinant yeast cell comprising:

a nucleic acid construct according to Claim 23 or Claim 24.

26. The recombinant yeast cell according to Claim 25, wherein said yeast cell is a *Saccharomyces* cell.

27. A recombinant yeast cell comprising:

at least one copy of a vector comprising a fungal nucleotide sequence which encodes a polypeptide which converts 18:2 fatty acids to 18:3 fatty acids or 18:3 fatty acids to 18:4 fatty acids, wherein said yeast cell or an ancestor of said yeast cell was transformed with said vector to produce said recombinant yeast cell, and wherein said nucleotide sequence is operably associated with an expression control sequence functional in said recombinant yeast cell.

28. The recombinant yeast cell according to claim 27, wherein said fungal nucleotide sequence is a *Mortierella* nucleotide sequence.

5 29. The recombinant yeast cell according to Claim 28, wherein said recombinant yeast cell is a *Saccharomyces* cell.

30. The microbial cell according to Claim 27, wherein said expression control sequence is provided in said expression vector.

10 31. A method for production of GLA in a yeast culture, said method comprising:

growing a yeast culture having a plurality of recombinant yeast cells, wherein said yeast cells or an ancestor of said yeast cells were transformed with a vector comprising fungal DNA encoding a polypeptide which converts LA to GLA, wherein said DNA is operably associated with an expression control sequence functional in said yeast cells, under conditions whereby said DNA is expressed, whereby GLA is produced from LA in said yeast culture.

15 32. The method according to Claim 31, wherein said fungal DNA is *Mortierella* DNA and said polypeptide is a $\Delta 6$ desaturase.

20 33. The method according to Claim 32, wherein *Mortierella* is of the species *Mortierella alpina*.

25 34. The method according to Claim 31, wherein said LA is exogenously supplied.

35. The method according to Claim 31, wherein said conditions are inducible.

5 36. A method for production of stearidonic acid in a yeast culture, said method comprising:

growing a yeast culture having a plurality of recombinant yeast cells, wherein said yeast cells or an ancestor of said yeast cells were transformed with a vector comprising fungal DNA encoding a polypeptide which converts α -linolenic acid to stearidonic acid, wherein said DNA is operably associated with an expression control sequence functional in said yeast cells, under conditions whereby said DNA is expressed, whereby stearidonic acid is produced from α -linolenic acid in said yeast culture.

10 37. The method according to Claim 36, wherein said fungal DNA is *Mortierella* DNA and said polypeptide is a $\Delta 6$ desaturase.

15 38. The method according to Claim 37, wherein *Mortierella* is of the species *Mortierella alpina*.

20 39. The method according to Claim 36, wherein said α -linolenic acid is exogenously supplied.

40. The method according to Claim 36, wherein said conditions are inducible.

25 41. A method for production of linoleic acid in a yeast culture, said method comprising:

growing a yeast culture having a plurality of recombinant yeast cells,
wherein said yeast cells or an ancestor of said yeast cells were transformed with a
vector comprising fungal DNA encoding a polypeptide which converts oleic acid to
linoleic acid, wherein said DNA is operably associated with an expression control
sequence functional in said yeast cells, under conditions whereby said DNA is
expressed, whereby linoleic acid is produced from oleic acid in said yeast culture.

42. The method according to Claim 41, wherein said fungal DNA is
Mortierella DNA and said polypeptide is a $\Delta 12$ desaturase.

43. The method according to Claim 42, wherein *Mortierella* is of the
species *Mortierella alpina*.

44. The method according to Claim 41, wherein said conditions are
inducible.

45. An isolated or purified polypeptide which desaturates a fatty acid
molecule at carbon 12 from the carboxyl end of said polypeptide, wherein said
polypeptide is a fungal polypeptide or is derived from a fungal polypeptide.

46. The isolated or purified polypeptide according to Claim 46, wherein
said polypeptide is a *Mortierella alpina* $\Delta 12$ desaturase.

47. An isolated or purified polypeptide which desaturates a fatty acid
molecule at carbon 6 from the carboxyl end of said polypeptide, wherein said
polypeptide is a fungal polypeptide or is derived from a fungal polypeptide.

48. The isolated or purified polypeptide according to Claim 48, wherein said polypeptide is a $\Delta 6$ desaturase.

5 49. An isolated nucleic acid encoding a polypeptide according to Claim 47 or Claim 49.

50. The nucleic acid construct according to Claim 23, wherein said portion of an amino acid sequence depicted in SEQ.ID. NO: 2 comprises amino acids 1 through 457.

10 51. A host cell comprising:

a nucleic acid construct according to any one of Claims 22 to 24.

52. A host cell comprising:

15 a vector which includes a nucleic acid which encodes a fatty acid desaturase derived from *Mortierella alpina*, wherein said desaturase has an amino acid sequence represented by SEQ ID NO:2, and wherein said nucleotide sequence is operably linked to a promoter.

20 53. The host cell according to Claim 52, wherein said host cell is a eukaryotic cell.

54. The host cell according to Claim 53, wherein said eukaryotic cell is selected from the group consisting of a mammalian cell, a plant cell, an insect cell, a fungal cell, an avian cell and an algal cell.

25 55. The host cell according to Claim 54, wherein said host cell is a fungal cell.

56. The host cell of Claim 21, wherein said promoter is exogenously supplied to said host cell.

5 57. A method for production of stearidonic acid in a eukaryotic cell culture, said method comprising:

growing a eukaryotic cell culture having a plurality of recombinant eukaryotic cells, wherein said recombinant eukaryotic cells or ancestors of said recombinant eukaryotic cells were transformed with a vector comprising fungal
10 DNA encoding a polypeptide which converts α -linolenic acid to stearidonic acid, wherein said DNA is operably associated with an expression control sequence functional in said recombinant eukaryotic cells, under conditions whereby said DNA is expressed, whereby stearidonic acid is produced from α -linolenic acid in said eukaryotic cell culture.

15 58. A method for production of linoleic acid in a eukaryotic cell culture, said method comprising:

growing a eukaryotic cell culture having a plurality of recombinant eukaryotic cells, wherein said recombinant eukaryotic cells or ancestors of said
20 recombinant eukaryotic cells were transformed with a vector comprising fungal DNA encoding a polypeptide which converts oleic acid to linoleic acid, wherein said DNA is operably associated with an expression control sequence functional in said recombinant eukaryotic cells, under conditions whereby said DNA is expressed, whereby linoleic acid is produced from oleic acid in said eukaryotic cell culture.

25 59. The method according to Claim 57 or Claim 58, wherein said eukaryotic cells are selected from the group consisting of mammalian cells, plant cells, insect cells, fungal cells, avian cells and algal cells.

60. The method according to Claim 59, wherein said fungal cells are yeast cells of the genus *Saccharomyces*.

61. A recombinant yeast cell comprising:

- 5 (1) at least one nucleic acid construct according to Claim 23 or 24; or
- (2) at least one nucleic acid construct according to Claim 23 and at least one nucleic acid construct according to Claim 24.

62. A recombinant yeast cell comprising:

- 10 at least one nucleic acid construct comprising a nucleotide sequence which encodes a functionally active $\Delta 6$ desaturase having an amino acid sequence which corresponds to or is complementary to all or a portion of an amino acid sequence depicted in SEQ ID NO: 2, and at least one nucleic acid construct comprising a
- 15 nucleotide sequence which encodes a functionally active $\Delta 12$ desaturase having an amino acid sequence which corresponds to or is complementary to all or a portion of an amino acid sequence depicted in SEQ ID NO: 4, wherein said nucleic acid constructs are operably associated with transcription control sequences functional in a yeast cell.

20 63. A method of making GLA, said method comprising:

 growing a recombinant yeast cell according to Claim 62 under conditions whereby said nucleotide sequences are expressed , whereby GLA is produced in said yeast cell.

25 64. A method of making GLA, said method comprising:

 growing a recombinant yeast cell according to Claim 61 under conditions whereby the nucleotide sequences in said nucleic acid constructs are expressed , whereby GLA is produced in said yeast cell.

65. A method for obtaining altered long chain polyunsaturated fatty acid biosynthesis comprising the steps of:

growing a plant having cells which contain one or more transgenes, derived from a fungus or algae, which encodes a transgene expression product which desaturates a fatty acid molecule at a carbon selected from the group consisting of carbon 6 and carbon 12 from the carboxyl end of said fatty acid molecule, wherein said one or more transgenes is operably associated with an expression control sequence, under conditions whereby said one or more transgenes is expressed, whereby long chain polyunsaturated fatty acid biosynthesis in said cells is altered.

66. The method according to claim 65, wherein said long chain polyunsaturated fatty acid is selected from the group consisting of 18:1 ω 9, LA, GLA, SDA and ALA.

67. A microbial oil or fraction thereof produced according to the method of claim 65.

68. A method of treating or preventing malnutrition comprising administering said microbial oil of claim 67 to a patient in need of said treatment or prevention in an amount sufficient to effect said treatment or prevention.

69. A pharmaceutical composition comprising said microbial oil or fraction of claim 67 and a pharmaceutically acceptable carrier.

70. The pharmaceutical composition of claim 69, wherein said pharmaceutical composition is in the form of a solid or a liquid.

71. The pharmaceutical composition of claim 70, wherein said pharmaceutical composition is in a capsule or tablet form.

72. The pharmaceutical composition of claim 69 further comprising at least one nutrient selected from the group consisting of a vitamin, a mineral, a carbohydrate, a sugar, an amino acid, a free fatty acid, a phospholipid, an antioxidant, and a phenolic compound.

73. A nutritional formula comprising said microbial oil or fraction thereof of claim 67.

74. The nutritional formula of claim 73, wherein said nutritional formula is selected from the group consisting of an infant formula, a dietary supplement, and a dietary substitute.

75. The nutritional formula of claim 74, wherein said infant formula, dietary supplement or dietary supplement is in the form of a liquid or a solid.

76. An infant formula comprising said microbial oil or fraction thereof of claim 67.

77. The infant formula of claim 76 further comprising at least one macronutrient selected from the group consisting of coconut oil, soy oil, canola oil, mono- and diglycerides, glucose, edible lactose, electrodialysed whey, electrodialysed skim milk, milk whey, soy protein, and other protein hydrolysates.

78. The infant formula of claim 77 further comprising at least one vitamin selected from the group consisting of Vitamins A, C, D, E, and B complex; and at least one mineral selected from the group consisting of calcium, magnesium, zinc, manganese, sodium, potassium, phosphorus, copper, chloride, iodine, selenium, and iron.

79. A dietary supplement comprising said microbial oil or fraction thereof of claim 67.

5 80. The dietary supplement of claim 79 further comprising at least one macronutrient selected from the group consisting of coconut oil, soy oil, canola oil, mono- and diglycerides, glucose, edible lactose, electro dialysed whey, electro dialysed skim milk, milk whey, soy protein, and other protein hydrolysates.

10 81. The dietary supplement of claim 80 further comprising at least one vitamin selected from the group consisting of Vitamins A, C, D, E, and B complex; and at least one mineral selected from the group consisting of calcium, magnesium, zinc, manganese, sodium, potassium, phosphorus, copper, chloride, iodine, selenium, and iron.

15 82. The dietary supplement of claim 79 or claim 81, wherein said dietary supplement is administered to a human or an animal.

20 83. A dietary substitute comprising said microbial oil or fraction thereof of claim 67.

25 84. The dietary substitute of claim 83 further comprising at least one macronutrient selected from the group consisting of coconut oil, soy oil, canola oil, mono- and diglycerides, glucose, edible lactose, electro dialysed whey, electro dialysed skim milk, milk whey, soy protein, and other protein hydrolysates.

85. The dietary substitute of claim 84 further comprising at least one vitamin selected from the group consisting of Vitamins A, C, D, E, and B complex; and at least one mineral selected from the group consisting of calcium, magnesium,

zinc, manganese, sodium, potassium, phosphorus, copper, chloride, iodine, selenium, and iron.

86. The dietary substitute of claim 83 or claim 85, wherein said dietary substitute is administered to a human or animal.

87. A method of treating a patient having a condition caused by insufficient intake or production of polyunsaturated fatty acids comprising administering to said patient said dietary substitute of claim 83 or said dietary supplement of claim 79 in an amount sufficient to effect said treatment.

88. The method of claim 87, wherein said dietary substitute or said dietary supplement is administered enterally or parenterally.

89. A cosmetic comprising said microbial oil or fraction thereof of claim 67.

90. The cosmetic of claim 88, wherein said cosmetic is applied topically.

91. The pharmaceutical composition of claim 69, wherein said pharmaceutical composition is administered to a human or an animal.

92. An animal feed comprising said microbial oil or fraction thereof of claim 67.

93. The method of claim 20 wherein said fungus is *Mortierella species*.

94. The method of claim 93 wherein said fungus is *Mortierella alpina*.

95. An isolated peptide sequence selected from the group consisting of SEQ ID NO:34 - SEQ ID NO:40.

5

96. An isolated peptide sequence selected from the group consisting of SEQ ID NO:20, SEQ ID NO:22, SEQ ID NO:25 and SEQ ID NO:26.

97. A method for production of gamma-linolenic acid in a eukaryotic cell culture, said method comprising:

growing a eukaryotic cell culture having a plurality of recombinant eukaryotic cells, wherein said recombinant eukaryotic cells or ancestors of said recombinant eukaryotic cells were transformed with a vector comprising fungal DNA encoding a polypeptide which converts linoleic acid to gamma-linolenic acid, wherein said DNA is operably associated with an expression control sequence functional in said recombinant eukaryotic cells, under conditions whereby said DNA is expressed, whereby gamma-linolenic acid is produced from linoleic acid in said eukaryotic cell culture.

98. The method according to Claim 97 wherein said eukaryotic cells are selected from the group consisting of mammalian cells, plant cells, insect cells, fungal cells, avian cells and algal cells.

20

SEQUENCE LISTING

5 (1) GENERAL INFORMATION:

(i) APPLICANT: KNUTZON, DEBORAH
MURKERJI, PRADIP
10 HUANG, YUNG-SHENG
THURMOND, JENNIFER
CHAUDHARY, SUNITA
LEONARD, AMANDA

15 (ii) TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR SYNTHESIS
OF LONG CHAIN POLY-UNSATURATED FATTY ACIDS

(iii) NUMBER OF SEQUENCES: 40

20 (iv) CORRESPONDENCE ADDRESS:
(A) ADDRESSEE: LIMBACH AND LIMBACH LLP
(B) STREET: 2001 FERRY BUILDING
(C) CITY: SAN FRANCISCO
(D) STATE: CA
25 (E) COUNTRY: USA
(F) ZIP: 94111

(v) COMPUTER READABLE FORM:
30 (A) MEDIUM TYPE: Floppy disk
(B) COMPUTER: IBM PC compatible
(C) OPERATING SYSTEM: PC-DOS/MS-DOS
(D) SOFTWARE: Microsoft Word

(vi) CURRENT APPLICATION DATA:
35 (A) APPLICATION NUMBER:
(B) (B) FILING DATE:
(C) CLASSIFICATION:

(viii) ATTORNEY/AGENT INFORMATION:
40 (A) NAME: WARD, MICHAEL R.
(B) REGISTRATION NUMBER: 38,651
(C) REFERENCE/DOCKET NUMBER: CGAB-210

(ix) TELECOMMUNICATION INFORMATION:
45 (A) TELEPHONE: (415) 433-4150
(B) TELEFAX: (415) 433-8716
(C) TELEX: N/A

50 (2) INFORMATION FOR SEQ ID NO:1:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1617 base pairs
(B) TYPE: nucleic acid
55 (C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

60 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

CGACACTCCT TCCTTCTTCT CACCCGTCCT AGTCCCCTTC AACCCCCCTC TTTGACAAAG 60
 ACAACAAACC ATGGCTGCTG CTCCCAGTGT GAGGACGTTT ACTCGGGCCG AGGTTTTGAA 120
 5 TGCCGAGGCT CTGAATGAGG GCAAGAAGGA TGCCGAGGCA CCCTTCTTGA TGATCATCGA 180
 CAACAAGGTG TACGATGTCC GCGAGTTCGT CCCTGATCAT CCCGGTGGAA GTGTGATTCT 240
 10 CACGCACGTT GGCAAGGACG GCACTGACGT CTTTGACACT TTTCACCCCG AGGCTGCTTG 300
 GGAGACTCTT GCCAACTTTT ACGTTGGTGA TATTGACGAG AGCGACCGCG ATATCAAGAA 360
 TGATGACTTT GCGGCCGAGG TCCGCAAGCT GCGTACCTTG TTCCAGTCTC TTGGTTACTA 420
 15 CGATTCTTCC AAGGCATACT ACGCCTTCAA GGTCTCGTTC AACCTCTGCA TCTGGGGTTT 480
 GTCGACGGTC ATTGTGGCCA AGTGGGGCCA GACCTCGACC CTCGCCAACG TGCTCTCGGC 540
 20 TGCGCTTTTG GGTCTGTCTT GGCAGCAGTG CGGATGGTTG GCTCAGACT TTTTGCATCA 600
 CCAGGTCTTC CAGGACCGTT TCTGGGGTGA TCTTTTCGGC GCCTTCTTGG GAGGTGTCTG 660
 CCAGGGCTTC TCGTCTCGT GGTGGAAGGA CAAGCACAAC ACTCACCACG CCGCCCCCAA 720
 25 CGTCCACGGC GAGGATCCCG ACATTGACAC CCACCCTCTG TTGACCTGGA GTGAGCATGC 780
 GTTGGAGATG TTCTCGGATG TCCCAGATGA GGAGCTGACC CGCATGTGGT CGCGTTTCAT 840
 30 GGTCTGAAC CAGACCTGGT TTTACTTCCC CATCTCTCG TTTGCCCGTC TCTCTGGTG 900
 CCTCCAGTCC ATTCTCTTTG TGCTGCCTAA CGGTCAGGCC CACAAGCCCT CGGGCGCGCG 960
 TGTGCCCATC TCGTTGGTCG AGCAGCTGTC GCTTGCGATG CACTGGACCT GGTACCTCGC 1020
 35 CACCATGTTC CTGTTTCATCA AGGATCCCGT CAACATGCTG GTGTACTTTT TGGTGTGCGA 1080
 GGCGGTGTGC GGAAACTTGT TGGCGATCGT GTTCTCGCTC AACCACAACG GTATGCCTGT 1140
 40 GATCTCGAAG GAGGAGCGG TCGATATGGA TTTCTTCACG AAGCAGATCA TCACGGGTGCG 1200
 TGATGTCCAC CCGGGTCTAT TTGCCAACTG GTTCACGGGT GGATTGAACT ATCAGATCGA 1260
 GCACCACTTG TTCCCTTCGA TGCCTCGCCA CAACCTTTTCA AAGATCCAGC CTGCTGTGCA 1320
 45 GACCCTGTGC AAAAAGTACA ATGTCCGATA CCACACCACC GGTATGATCG AGGGAACGTC 1380
 AGAGGTCTTT AGCCGTCTGA ACGAGGTCTC CAAGGCTGCC TCCAAGATGG GTAAGGCGCA 1440
 50 GTAAAAAAA AAACAAGGAC GTTTTTTTTC GCCAGTGCCT GTGCCTGTGC CTGCTTCCCT 1500
 TGTCAAGTCG AGCGTTTCTG GAAAGGATCG TTCAGTGCAG TATCATCATT CTCCTTTTAC 1560
 CCCCCGCTCA TATCTCATTC ATTTCTCTTA TTAAACAAC TGTTCCCCC TTCACCG 1617

(2) INFORMATION FOR SEQ ID NO:2:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 457 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS: not relevant

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

5 Met Ala Ala Ala Pro Ser Val Arg Thr Phe Thr Arg Ala Glu Val Leu
1 . 5 10 15

Asn Ala Glu Ala Leu Asn Glu Gly Lys Lys Asp Ala Glu Ala Pro Phe
20 25 30

10 Leu Met Ile Ile Asp Asn Lys Val Tyr Asp Val Arg Glu Phe Val Pro
35 40 45

15 Asp His Pro Gly Gly Ser Val Ile Leu Thr His Val Gly Lys Asp Gly
50 55 60

Thr Asp Val Phe Asp Thr Phe His Pro Glu Ala Ala Trp Glu Thr Leu
65 70 75 80

20 Ala Asn Phe Tyr Val Gly Asp Ile Asp Glu Ser Asp Arg Asp Ile Lys
85 90 95

Asn Asp Asp Phe Ala Ala Glu Val Arg Lys Leu Arg Thr Leu Phe Gln
100 105 110

25 Ser Leu Gly Tyr Tyr Asp Ser Ser Lys Ala Tyr Tyr Ala Phe Lys Val
115 120 125

30 Ser Phe Asn Leu Cys Ile Trp Gly Leu Ser Thr Val Ile Val Ala Lys
130 135 140

Trp Gly Gln Thr Ser Thr Leu Ala Asn Val Leu Ser Ala Ala Leu Leu
145 150 155 160

35 Gly Leu Phe Trp Gln Gln Cys Gly Trp Leu Ala His Asp Phe Leu His
165 170 175

His Gln Val Phe Gln Asp Arg Phe Trp Gly Asp Leu Phe Gly Ala Phe
180 185 190

40 Leu Gly Gly Val Cys Gln Gly Phe Ser Ser Ser Trp Trp Lys Asp Lys
195 200 205

45 His Asn Thr His His Ala Ala Pro Asn Val His Gly Glu Asp Pro Asp
210 215 220

Ile Asp Thr His Pro Leu Leu Thr Trp Ser Glu His Ala Leu Glu Met
225 230 235 240

50 Phe Ser Asp Val Pro Asp Glu Glu Leu Thr Arg Met Trp Ser Arg Phe
245 250 255

Met Val Leu Asn Gln Thr Trp Phe Tyr Phe Pro Ile Leu Ser Phe Ala
260 265 270

55 Arg Leu Ser Trp Cys Leu Gln Ser Ile Leu Phe Val Leu Pro Asn Gly
275 280 285

60 Gln Ala His Lys Pro Ser Gly Ala Arg Val Pro Ile Ser Leu Val Glu
290 295 300

Gln Leu Ser Leu Ala Met His Trp Thr Trp Tyr Leu Ala Thr Met Phe
305 310 315 320

65 Leu Phe Ile Lys Asp Pro Val Asn Met Leu Val Tyr Phe Leu Val Ser

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SUBSTITUTE SHEET

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GCCGTTTCAGG AGGAGGACAT GTCCGTGCAC CTGGATGAGG AGGCTCCCAT TGTGACTTTG 780
 TTCTGGATGG TGATCCAGTT CTTGTTCGGA TGGCCCGCGT ACCTGATTAT GAACGCCTCT 840
 GGCCAAGACT ACGGCCGCTG GACCTCGCAC TTCCACACGT ACTCGCCCAT CTTTGAGCCC 900
 CGCAACTTTT TCGACATTAT TATCTCGGAC CTCGGTGTGT TGGCTGCCCT CGGTGCCCTG 960
 ATCTATGCCT CCATGCAGTT GTCGCTCTTG ACCGTCACCA AGTACTATAT TGTCCCCTAC 1020
 CTCTTTGTCA ACTTTTGGTT GGTCTGATC ACCTTCTTGC AGCACACCGA TCCCAAGCTG 1080
 CCCCATTACC GCGAGGGTGC CTGGAATTTT CAGCGTGGAG CTCTTTGCAC CGTTGACCGC 1140
 TCGTTTGGCA AGTTCTTGGA CCATATGTTT CACGGCATTG TCCACACCCA TGTGGCCCAT 1200
 CACTTGTTCT CGCAAATGCC GTTCTACCAT GCTGAGGAAG CTACCTATCA TCTCAAGAAA 1260
 CTGCTGGGAG AGTACTATGT GTACGACCCA TCCCCGATCG TCGTTGCGGT CTGGAGGTCG 1320
 TTCCGTGAGT GCCGATTCTG GGAGGATCAG GGAGACGTGG TCTTTTTCAA GAAGTAAAAA 1380
 AAAAGACAAT GGACCACACA CAACCTTGTC TCTACAGACC TACGTATCAT GTAGCCATAC 1440
 CACTTCATAA AAGAACATGA GCTCTAGAGG CGTGTCAATC GCGCCTCC 1488

(2) INFORMATION FOR SEQ ID NO:4:

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 35
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 45
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(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 399 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: not relevant
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

Met	Ala	Pro	Pro	Asn	Thr	Ile	Asp	Ala	Gly	Leu	Thr	Gln	Arg	His	Ile	1	5	10	15
Ser	Thr	Ser	Ala	Pro	Asn	Ser	Ala	Lys	Pro	Ala	Phe	Glu	Arg	Asn	Tyr	20	25	30	
Gln	Leu	Pro	Glu	Phe	Thr	Ile	Lys	Glu	Ile	Arg	Glu	Cys	Ile	Pro	Ala	35	40	45	
His	Cys	Phe	Glu	Arg	Ser	Gly	Leu	Arg	Gly	Leu	Cys	His	Val	Ala	Ile	50	55	60	
Asp	Leu	Thr	Trp	Ala	Ser	Leu	Leu	Phe	Leu	Ala	Ala	Thr	Gln	Ile	Asp	65	70	75	80
Lys	Phe	Glu	Asn	Pro	Leu	Ile	Arg	Tyr	Leu	Ala	Trp	Pro	Val	Tyr	Trp	85	90	95	
Ile	Met	Gln	Gly	Ile	Val	Cys	Thr	Gly	Val	Trp	Val	Leu	Ala	His	Glu	100	105	110	
Cys	Gly	His	Gln	Ser	Phe	Ser	Thr	Ser	Lys	Thr	Leu	Asn	Asn	Thr	Val	115	120	125	

	Gly	Trp	Ile	Leu	His	Ser	Met	Leu	Leu	Val	Pro	Tyr	His	Ser	Trp	Arg	
	130						135					140					
5	Ile	Ser	His	Ser	Lys	His	His	Lys	Ala	Thr	Gly	His	Met	Thr	Lys	Asp	
	145					150					155					160	
	Gln	Val	Phe	Val	Pro	Lys	Thr	Arg	Ser	Gln	Val	Gly	Leu	Pro	Pro	Lys	
					165					170					175		
10	Glu	Asn	Ala	Ala	Ala	Ala	Val	Gln	Glu	Glu	Asp	Met	Ser	Val	His	Leu	
				180					185					190			
	Asp	Glu	Glu	Ala	Pro	Ile	Val	Thr	Leu	Phe	Trp	Met	Val	Ile	Gln	Phe	
		195						200					205				
15	Leu	Phe	Gly	Trp	Pro	Ala	Tyr	Leu	Ile	Met	Asn	Ala	Ser	Gly	Gln	Asp	
	210						215					220					
20	Tyr	Gly	Arg	Trp	Thr	Ser	His	Phe	His	Thr	Tyr	Ser	Pro	Ile	Phe	Glu	
	225					230					235					240	
	Pro	Arg	Asn	Phe	Phe	Asp	Ile	Ile	Ile	Ser	Asp	Leu	Gly	Val	Leu	Ala	
				245						250					255		
25	Ala	Leu	Gly	Ala	Leu	Ile	Tyr	Ala	Ser	Met	Gln	Leu	Ser	Leu	Leu	Thr	
			260						265					270			
	Val	Thr	Lys	Tyr	Tyr	Ile	Val	Pro	Tyr	Leu	Phe	Val	Asn	Phe	Trp	Leu	
			275					280					285				
30	Val	Leu	Ile	Thr	Phe	Leu	Gln	His	Thr	Asp	Pro	Lys	Leu	Pro	His	Tyr	
		290					295					300					
35	Arg	Glu	Gly	Ala	Trp	Asn	Phe	Gln	Arg	Gly	Ala	Leu	Cys	Thr	Val	Asp	
	305					310					315					320	
	Arg	Ser	Phe	Gly	Lys	Phe	Leu	Asp	His	Met	Phe	His	Gly	Ile	Val	His	
				325						330					335		
40	Thr	His	Val	Ala	His	His	Leu	Phe	Ser	Gln	Met	Pro	Phe	Tyr	His	Ala	
				340					345					350			
	Glu	Glu	Ala	Thr	Tyr	His	Leu	Lys	Lys	Leu	Leu	Gly	Glu	Tyr	Tyr	Val	
			355					360					365				
45	Tyr	Asp	Pro	Ser	Pro	Ile	Val	Val	Ala	Val	Trp	Arg	Ser	Phe	Arg	Glu	
	370						375					380					
50	Cys	Arg	Phe	Val	Glu	Asp	Gln	Gly	Asp	Val	Val	Phe	Phe	Lys	Lys		
	385					390					395						

(2) INFORMATION FOR SEQ ID NO:5:

- 55 (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 355 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: not relevant
 - (D) TOPOLOGY: linear
- 60 (ii) MOLECULE TYPE: peptide
- 65 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

	Glu	Val	Arg	Lys	Leu	Arg	Thr	Leu	Phe	Gln	Ser	Leu	Gly	Tyr	Tyr	Asp	
	1				5					10					15		
5	Ser	Ser	Lys	Ala	Tyr	Tyr	Ala	Phe	Lys	Val	Ser	Phe	Asn	Leu	Cys	Ile	
				20					25					30			
	Trp	Gly	Leu	Ser	Thr	Val	Ile	Val	Ala	Lys	Trp	Gly	Gln	Thr	Ser	Thr	
			35					40					45				
10	Leu	Ala	Asn	Val	Leu	Ser	Ala	Leu	Leu	Gly	Leu	Phe	Trp	Gln	Gln		
		50					55				60						
	Cys	Gly	Trp	Leu	Ala	His	Asp	Phe	Leu	His	His	Gln	Val	Phe	Gln	Asp	
15	65					70					75					80	
	Arg	Phe	Trp	Gly	Asp	Leu	Phe	Gly	Ala	Phe	Leu	Gly	Gly	Val	Cys	Gln	
					85					90					95		
20	Gly	Phe	Ser	Ser	Ser	Trp	Trp	Lys	Asp	Lys	His	Asn	Thr	His	His	Ala	
				100					105					110			
	Ala	Pro	Asn	Val	His	Gly	Glu	Asp	Pro	Asp	Ile	Asp	Thr	His	Pro	Leu	
25			115					120					125				
	Leu	Thr	Trp	Ser	Glu	His	Ala	Leu	Glu	Met	Phe	Ser	Asp	Val	Pro	Asp	
		130					135					140					
30	Glu	Glu	Leu	Thr	Arg	Met	Trp	Ser	Arg	Phe	Met	Val	Leu	Asn	Gln	Thr	
	145					150					155					160	
	Trp	Phe	Tyr	Phe	Pro	Ile	Leu	Ser	Phe	Ala	Arg	Leu	Ser	Trp	Cys	Leu	
					165					170					175		
35	Gln	Ser	Ile	Leu	Phe	Val	Leu	Pro	Asn	Gly	Gln	Ala	His	Lys	Pro	Ser	
				180					185					190			
	Gly	Ala	Arg	Val	Pro	Ile	Ser	Leu	Val	Glu	Gln	Leu	Ser	Leu	Ala	Met	
			195					200					205				
40	His	Trp	Thr	Trp	Tyr	Leu	Ala	Thr	Met	Phe	Leu	Phe	Ile	Lys	Asp	Pro	
		210					215					220					
	Val	Asn	Met	Leu	Val	Tyr	Phe	Leu	Val	Ser	Gln	Ala	Val	Cys	Gly	Asn	
45	225					230					235					240	
	Leu	Leu	Ala	Ile	Val	Phe	Ser	Leu	Asn	His	Asn	Gly	Met	Pro	Val	Ile	
				245						250					255		
50	Ser	Lys	Glu	Glu	Ala	Val	Asp	Met	Asp	Phe	Phe	Thr	Lys	Gln	Ile	Ile	
				260					265					270			
	Thr	Gly	Arg	Asp	Val	His	Pro	Gly	Leu	Phe	Ala	Asn	Trp	Phe	Thr	Gly	
			275					280					285				
55	Gly	Leu	Asn	Tyr	Gln	Ile	Glu	His	His	Leu	Phe	Pro	Ser	Met	Pro	Arg	
		290					295					300					
60	His	Asn	Phe	Ser	Lys	Ile	Gln	Pro	Ala	Val	Glu	Thr	Leu	Cys	Lys	Lys	
	305					310				315						320	
	Tyr	Asn	Val	Arg	Tyr	His	Thr	Thr	Gly	Met	Ile	Glu	Gly	Thr	Ala	Glu	
					325					330					335		
65	Val	Phe	Ser	Arg	Leu	Asn	Glu	Val	Ser	Lys	Ala	Ala	Ser	Lys	Met	Gly	

340

345

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Lys Ala Gln
355

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(2) INFORMATION FOR SEQ ID NO:6:

(i) SEQUENCE CHARACTERISTICS:

10

- (A) LENGTH: 104 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: not relevant
- (D) TOPOLOGY: linear

15

(ii) MOLECULE TYPE: peptide

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

Val Thr Leu Tyr Thr Leu Ala Phe Val Ala Ala Asn Ser Leu Gly Val
1 5 10 15

25

Leu Tyr Gly Val Leu Ala Cys Pro Ser Val Xaa Pro His Gln Ile Ala
20 25 30

Ala Gly Leu Leu Gly Leu Leu Trp Ile Gln Ser Ala Tyr Ile Gly Xaa
35 40 45

30

Asp Ser Gly His Tyr Val Ile Met Ser Asn Lys Ser Asn Asn Xaa Phe
50 55 60

35

Ala Gln Leu Leu Ser Gly Asn Cys Leu Thr Gly Ile Ile Ala Trp Trp
65 70 75 80

Lys Trp Thr His Asn Ala His His Leu Ala Cys Asn Ser Leu Asp Tyr
85 90 95

40

Gly Pro Asn Leu Gln His Ile Pro
100

(2) INFORMATION FOR SEQ ID NO:7:

(i) SEQUENCE CHARACTERISTICS:

45

- (A) LENGTH: 252 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: not relevant
- (D) TOPOLOGY: linear

50

(ii) MOLECULE TYPE: peptide

55

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

Gly Val Leu Tyr Gly Val Leu Ala Cys Thr Ser Val Phe Ala His Gln
1 5 10 15

60

Ile Ala Ala Ala Leu Leu Gly Leu Leu Trp Ile Gln Ser Ala Tyr Ile
20 25 30

Gly His Asp Ser Gly His Tyr Val Ile Met Ser Asn Lys Ser Tyr Asn
35 40 45

65

5 Arg Phe Ala Gln Leu Leu Ser Gly Asn Cys Leu Thr Gly Ile Ser Ile
 50 55 60
 Ala Trp Trp Lys Trp Thr His Asn Ala His His Leu Ala Cys Asn Ser
 65 70 75 80
 Leu Asp Tyr Asp Pro Asp Leu Gln His Ile Pro Val Phe Ala Val Ser
 85 90 95
 10 Thr Lys Phe Phe Ser Ser Leu Thr Ser Arg Phe Tyr Asp Arg Lys Leu
 100 105 110
 Thr Phe Gly Pro Val Ala Arg Phe Leu Val Ser Tyr Gln His Phe Thr
 15 115 120 125
 Tyr Tyr Pro Val Asn Cys Phe Gly Arg Ile Asn Leu Phe Ile Gln Thr
 130 135 140
 20 Phe Leu Leu Leu Phe Ser Lys Arg Glu Val Pro Asp Arg Ala Leu Asn
 145 150 155 160
 Phe Ala Gly Ile Leu Val Phe Trp Thr Trp Phe Pro Leu Leu Val Ser
 165 170 175
 25 Cys Leu Pro Asn Trp Pro Glu Arg Phe Phe Phe Val Phe Thr Ser Phe
 180 185 190
 Thr Val Thr Ala Leu Gln His Ile Gln Phe Thr Leu Asn His Phe Ala
 30 195 200 205
 Ala Asp Val Tyr Val Gly Pro Pro Thr Gly Ser Asp Trp Phe Glu Lys
 210 215 220
 35 Gln Ala Ala Gly Thr Ile Asp Ile Ser Cys Arg Ser Tyr Met Asp Trp
 225 230 235 240
 Phe Phe Gly Gly Leu Gln Phe Gln Leu Glu His His
 245 250

(2) INFORMATION FOR SEQ ID NO:8:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 125 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: not relevant
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

55 Gly Xaa Xaa Asn Phe Ala Gly Ile Leu Val Phe Trp Thr Trp Phe Pro
 1 5 10 15
 Leu Leu Val Ser Cys Leu Pro Asn Trp Pro Glu Arg Phe Xaa Phe Val
 60 20 25 30
 Phe Thr Gly Phe Thr Val Thr Ala Leu Gln His Ile Gln Phe Thr Leu
 35 40 45
 65 Asn His Phe Ala Ala Asp Val Tyr Val Gly Pro Pro Thr Gly Ser Asp
 50 55 60

5 Trp Phe Glu Lys Gln Ala Ala Gly Thr Ile Asp Ile Ser Cys Arg Ser
 65 70 75 80
 Tyr Met Asp Trp Phe Phe Cys Gly Leu Gln Phe Gln Leu Glu His His
 85 90 95
 10 Leu Phe Pro Arg Leu Pro Arg Cys His Leu Arg Lys Val Ser Pro Val
 100 105 110
 Gly Gln Arg Gly Phe Gln Arg Lys Xaa Asn Leu Ser Xaa
 115 120 125

(2) INFORMATION FOR SEQ ID NO:9:

- 15 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 131 amino acids
 (B) TYPE: amino acid
 20 (C) STRANDEDNESS: not relevant
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

30 Pro Ala Thr Glu Val Gly Gly Leu Ala Trp Met Ile Thr Phe Tyr Val
 1 5 10 15
 Arg Phe Phe Leu Thr Tyr Val Pro Leu Leu Gly Leu Lys Ala Phe Leu
 20 25 30
 35 Gly Leu Phe Phe Ile Val Arg Phe Leu Glu Ser Asn Trp Phe Val Trp
 35 40 45
 Val Thr Gln Met Asn His Ile Pro Met His Ile Asp His Asp Arg Asn
 50 55 60
 40 Met Asp Trp Val Ser Thr Gln Leu Gln Ala Thr Cys Asn Val His Lys
 65 70 75 80
 Ser Ala Phe Asn Asp Trp Phe Ser Gly His Leu Asn Phe Gln Ile Glu
 85 90 95
 45 His His Leu Phe Pro Thr Met Pro Arg His Asn Tyr His Xaa Val Ala
 100 105 110
 50 Pro Leu Val Gln Ser Leu Cys Ala Lys His Gly Ile Glu Tyr Gln Ser
 115 120 125
 Lys Pro Leu
 130

(2) INFORMATION FOR SEQ ID NO:10:

- 60 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 87 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: not relevant
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

5 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

Cys Ser Pro Lys Ser Ser Pro Thr Arg Asn Met Thr Pro Ser Pro Phe
1 5 10 15

Ile Asp Trp Leu Trp Gly Gly Leu Asn Tyr Gln Ile Glu His His Leu
20 25 30

Phe Pro Thr Met Pro Arg Cys Asn Leu Asn Arg Cys Met Lys Tyr Val
35 40 45

15 Lys Glu Trp Cys Ala Glu Asn Asn Leu Pro Tyr Leu Val Asp Asp Tyr
50 55 60

Phe Val Gly Tyr Asn Leu Asn Leu Gln Gln Leu Lys Asn Met Ala Glu
65 70 75 80

20 Leu Val Gln Ala Lys Ala Ala
85

25 (2) INFORMATION FOR SEQ ID NO:11:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 143 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: not relevant
30 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

35 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:

Arg His Glu Ala Ala Arg Gly Gly Thr Arg Leu Ala Tyr Met Leu Val
40 1 5 10 15

Cys Met Gln Trp Thr Asp Leu Leu Trp Ala Ala Ser Phe Tyr Ser Arg
20 25 30

45 Phe Phe Leu Ser Tyr Ser Pro Phe Tyr Gly Ala Thr Gly Thr Leu Leu
35 40 45

Leu Phe Val Ala Val Arg Val Leu Glu Ser His Trp Phe Val Trp Ile
50 55 60

Thr Gln Met Asn His Ile Pro Lys Glu Ile Gly His Glu Lys His Arg
65 70 75 80

55 Asp Trp Ala Ser Ser Gln Leu Ala Ala Thr Cys Asn Val Glu Pro Ser
85 90 95

Leu Phe Ile Asp Trp Phe Ser Gly His Leu Asn Phe Gln Ile Glu His
100 105 110

60 His Leu Phe Pro Thr Met Thr Arg His Asn Tyr Arg Xaa Val Ala Pro
115 120 125

Leu Val Lys Ala Phe Cys Ala Lys His Gly Leu His Tyr Glu Val
130 135 140

65

(2) INFORMATION FOR SEQ ID NO:12:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 35 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:12:

CCAAGCTTCT GCAGGAGCTC TTTTTTTTTT TTTT

35

(2) INFORMATION FOR SEQ ID NO:13:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 33 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:13:

CUACUACUAC UAGGAGTCCT CTACGGTGTT TTG

33

(2) INFORMATION FOR SEQ ID NO:14:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 33 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:14:

CAUCAUCAUC AUATGATGCT CAAGCTGAAA CTG

33

(2) INFORMATION FOR SEQ ID NO:15:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 39 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:15:

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TACCAACTCG AGAAAATGGC TGCTGCTCCC AGTGTGAGG

39

(2) INFORMATION FOR SEQ ID NO:16:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 39 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:16:

AACTGATCTA GATTACTGCG CCTTACCCAT CTTGGAGGC

39

(2) INFORMATION FOR SEQ ID NO:17:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 39 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:17:

TACCAACTCG AGAAAATGGC ACCTCCCAAC ACTATCGAT

39

(2) INFORMATION FOR SEQ ID NO:18:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 39 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:18:

AACTGATCTA GATTACTTCT TGAAAAAGAC CACGTCTCC

39

(2) INFORMATION FOR SEQ ID NO:19:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 746 nucleic acids
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: not relevant
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: nucleic acid

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:19:

5 CGTATGTCAC TCCATTCCAA ACTCGTTCAT GGTATCATAA ATATCAACAC ATTTACGCTC 60
CACTCCTCTA TGGTATTTAC AACTCAAAT ATCGTACTCA AGATTGGGAA GCTTTTGTA 120
AGGATGGTAA AAATGGTGCA ATTCGTGTTA GTGTCGCCAC AAATTTCGAT AAGGCCGCTT 180
ACGTCATTGG TAAATTGTCT TTTGTTTTCT TCCGTTTCAT CCTTCCACTC CGTTATCATA 240
GCTTTACAGA TTTAATTTGT TATTTCTCA TCGCTGAATT CGTCTTTGGT TGGTATCTCA 300
CAATTAATTT CCAAGTTAGT CATGTCGCTG AAGATCTCAA ATTCTTTGCT ACCCCTGAAA 360
10 GACCAGATGA ACCATCTCAA ATCAATGAAG ATTGGGCAAT CCTTCAACTT AAAACTACTC 420
AAGATTATGG TCATGGTTCA CTCCTTTGTA CCTTTTGTAG TGGTCTTTA AATCATCAAG 480
TTGTTTCATCA TTTATTTCCA TCAATTGCTC AAGATTTCTA CCCACAACCT GTACCAATTG 540
TAAAAGAAGT TTGTAAAGAA CATAACATTA CTTACCACAT TAAACCAAAC TTCCTGAAG 600
CTATTATGTC ACACATTAAT TACCTTTACA AAATGGGTAA TGATCCAGAT TATGTTAAAA 660
15 AACCATTAGC CTCAAAGAT GATTAAATGA AATAACTTAA AAACCAATTA TTTACTTTTG 720
ACAAACAGTA ATATTAATAA ATACAA 746

(2) INFORMATION FOR SEQ ID NO:20:

20 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 227 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: not relevant
25 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:20:

30 Tyr Val Thr Pro Phe Gln Thr Arg Ser Trp Tyr His Lys Tyr Gln
1 5 10 15
His Ile Tyr Ala Pro Leu Leu Tyr Gly Ile Tyr Thr Leu Lys Tyr
20 25 30
35 Arg Thr Gln Asp Trp Glu Ala Phe Val Lys Asp Gly Lys Asn Gly
35 40 45
Ala Ile Arg Val Ser Val Ala Thr Asn Phe Asp Lys Ala Ala Tyr
50 55 60
Val Ile Gly Lys Leu Ser Phe Val Phe Phe Arg Phe Ile Leu Pro
65 70 75
40 Leu Arg Tyr His Ser Phe Thr Asp Leu Ile Cys Tyr Phe Leu Ile
80 85 90
Ala Glu Phe Val Phe Gly Trp Tyr Leu Thr Ile Asn Phe Gln Val
95 100 105
45 Ser His Val Ala Glu Asp Leu Lys Phe Phe Ala Thr Pro Glu Arg
110 115 120
Pro Asp Glu Pro Ser Gln Ile Asn Glu Asp Trp Ala Ile Leu Gln
125 130 135
Leu Lys Thr Thr Gln Asp Tyr Gly His Gly Ser Leu Leu Cys Thr
140 145 150
50 Phe Phe Ser Gly Ser Leu Asn His Gln Val Val His His Leu Phe
155 160 165
Pro Ser Ile Ala Gln Asp Phe Tyr Pro Gln Leu Val Pro Ile Val
170 175 180
55 Lys Glu Val Cys Lys Glu His Asn Ile Thr Tyr His Ile Lys Pro
185 190 195
Asn Phe Thr Glu Ala Ile Met Ser His Ile Asn Tyr Leu Tyr Lys
200 205 210
Met Gly Asn Asp Pro Asp Tyr Val Lys Lys Pro Leu Ala Ser Lys
215 220 225
60 Asp Asp Xaa

(2) INFORMATION FOR SEQ ID NO 21:

65 (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 494 nucleic acids
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: not relevant
 (D) TOPOLOGY: linear

5

(ii) MOLECULE TYPE: nucleic acid

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:21:

10

TTTTGGAAGG	NTCCAAGTTN	ACCACGGANT	NGGCAAGTTN	ACGGGGCGGA	AANCGGTTTT	60
CCCCCAAGC	CTTTTGTGCA	CTGGTTCTGT	GGTGGCTTCC	AGTACCAAGT	CGACCACCAC	120
TTATTCCCCA	GCCTGCCCCG	ACACAATCTG	GCCAAGACAC	ACGCACTGGT	CGAATCGTTC	180
TGCAAGGAGT	GGGGTGTCCA	GTACCACGAA	GCCGACCTCG	TGGACGGGAC	CATGGAAGTC	240
TTGCACCATT	TGGGCAGCGT	GGCCGGCGAA	TTCGTCGTGG	ATTTTGTACG	CGACGGACCC	300
GCCATGTAAT	CGTCGTTCTG	GACGATGCAA	GGGTTACGCG	ACATCTACAC	ACACTCACTC	360
ACACAAC TAG	TGTAAC TCGT	ATAGAATTCG	GTGTCGACCT	GGACCTTGTT	TGACTGGTTG	420
GGGATAGGGT	AGGTAGGCGG	ACGCGTGGGT	CGNCCCCGGG	AATTCTGTGA	CCGGTACCTG	480
CCCCGCGTNA	AAGT					494

20

(2) INFORMATION FOR SEQ ID NO:22:

25

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 87 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: not relevant
 (D) TOPOLOGY: linear

30

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:22:

35

Phe	Trp	Lys	Xaa	Pro	Ser	Xaa	Pro	Arg	Xaa	Xaa	Gln	Val	Xaa	Gly	1	5	10	15
Ala	Glu	Xaa	Gly	Phe	Pro	Pro	Lys	Pro	Phe	Val	Asp	Trp	Phe	Cys	20	25	30	35
Gly	Gly	Phe	Gln	Tyr	Gln	Val	Asp	His	His	Leu	Phe	Pro	Ser	Leu	40	45	50	55
Pro	Arg	His	Asn	Leu	Ala	Lys	Thr	His	Ala	Leu	Val	Glu	Ser	Phe	60	65	70	75
Cys	Lys	Glu	Trp	Gly	Val	Gln	Tyr	His	Glu	Ala	Asp	Leu	Val	Asp	80	85		
Gly	Thr	Met	Glu	Val	Leu	His	His	Leu	Gly	Ser	Val	Ala	Gly	Glu				
Phe	Val	Val	Asp	Phe	Val	Arg	Asp	Gly	Pro	Ala	Met							

50

55

(2) INFORMATION FOR SEQ ID NO:23:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 520 nucleic acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: not relevant
 (D) TOPOLOGY: linear

60

(ii) MOLECULE TYPE: nucleic acid

65

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:23:

5 GGATGGAGTT CGTCTGGATC GCTGTGCGCT ACGCGACGTG GTTTAAGCGT CATGGGTGCG 60
 CTTGGGTACA CGCCGGGGCA GTCGTTGGGC ATGTACTTGT GCGCCTTTGG TCTCGGCTGC 120
 ATTTACATTT TTCTGCAGTT CGCCGTAAAGT CACACCCATT TGCCCGTGAG CAACCCGGAG 180
 GATCAGCTGC ATTTGGCTCGA GTACGCGCGG ACCACACTGT GAACATCAGC ACCAAGTCGT 240
 GGTTCGTCAC ATGGTGGATG TCGAACCTCA ACTTTCAGAT CGAGCACCAC CTTTTCCCCA 300
 CGGCGCCCCA GTTCCGTTC AAGGAGATCA GCCCGCGCGT CGAGGCCCTC TTCAAGCGCC 360
 10 ACGGTCTCCC TTACTACGAC ATGCCCTACA CGAGCGCCGT CTCCACCACC TTTGCCAACC 420
 TCTACTCCGT CGGCCATTCC GTCGCGCAGC CCAAGCGCGA CTAGCCTCTT TTCCTAGACC 480
 TTAATTCCCC ACCCCACCCC ATGTTCTGTC TTCCTCCCGC 520

15 (2) INFORMATION FOR SEQ ID NO:24:
 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 153 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: not relevant
 (D) TOPOLOGY: linear
 (ii) MOLECULE TYPE: peptide
 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:24:

25
 30 Met Glu Phe Val Trp Ile Ala Val Arg Tyr Ala Thr Trp Phe Lys
 1 5 10 15
 Arg His Gly Cys Ala Trp Val His Ala Gly Ala Val Val Gly His
 20 25 30
 Val Leu Val Arg Leu Trp Ser Arg Leu His Leu His Phe Ser Ala
 35 40 45
 Val Arg Arg Lys Ser His Pro Phe Ala Arg Glu Gln Pro Gly Gly
 50 55 60
 Ser Ala Ala Leu Ala Arg Val Arg Ala Asp His Thr Val Asn Ile
 65 70 75
 Ser Thr Lys Ser Trp Phe Val Thr Trp Trp Met Ser Asn Leu Asn
 80 85 90
 40 Phe Gln Ile Glu His His Leu Phe Pro Thr Ala Pro Gln Phe Arg
 95 100 105
 Phe Lys Glu Ile Ser Pro Arg Val Glu Ala Leu Phe Lys Arg His
 110 115 120
 Gly Leu Pro Tyr Tyr Asp Met Pro Tyr Thr Ser Ala Val Ser Thr
 125 130 135
 45 Thr Phe Ala Asn Leu Tyr Ser Val Gly His Ser Val Gly Asp Ala
 140 145 150
 Lys Arg Asp

50 (2) INFORMATION FOR SEQ ID NO:25:
 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 420 nucleic acids
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: not relevant
 (D) TOPOLOGY: linear
 (ii) MOLECULE TYPE: nucleic acid
 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:25:

65 ACGCGTCCGC CCACGCGTCC GCCGCGAGCA ACTCATCAAG GAAGGCTACT TTGACCCCTC 60
 GCTCCCGCAC ATGACGTACC GCGTGGTCGA GATTGTTGTT CTCTTCGTGC TTTCCTTTTG 120

5 GCTGATGGGT CAGTCTTCAC CCCTCGCGCT CGCTCTCGGC ATTGTCGTCA GCGGCATCTC 180
 TCAGGGTCGC TCGGGCTGGG TAATGCATGA GATGGGCCAT GGGTCGTTCA CTGGTGTCAT 240
 TTGGCTTGAC GACCGGTTGT GCGAGTTCTT TTACGGCGTT GGTGTGGCA TGAGCGGTCA 300
 TTACTGGAAG AACACGACA GCAAACACCA CGCAGCGCCA AACCGGCTCG AGCACGATGT 360
 AGATCTCAAC ACCTTGCCAT TGGTGGCCTT CAACGAGCGC GTCGTGCGCA AGGTCCGACC 420

10 (2) INFORMATION FOR SEQ ID NO:26:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 125 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: not relevant
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:26:

25 Arg Val Arg Pro Arg Val Arg Arg Glu Gln Leu Ile Lys Glu Gly
 1 5 10 15
 Tyr Phe Asp Pro Ser Leu Pro His Met Thr Tyr Arg Val Val Glu
 20 25 30
 Ile Val Val Leu Phe Val Leu Ser Phe Trp Leu Met Gly Gln Ser
 35 40 45
 Ser Pro Leu Ala Leu Ala Leu Gly Ile Val Val Ser Gly Ile Ser
 50 55 60
 Gln Gly Arg Cys Gly Trp Val Met His Glu Met Gly His Gly Ser
 65 70 75
 Phe Thr Gly Val Ile Trp Leu Asp Asp Arg Leu Cys Glu Phe Phe
 80 85 90
 Tyr Gly Val Gly Cys Gly Met Ser Gly His Tyr Trp Lys Asn Gln
 95 100 105
 His Ser Lys His His Ala Ala Pro Asn Arg Leu Glu His Asp Val
 110 115 120
 Asp Leu Asn Thr Leu Pro Leu Val Ala Phe Asn Glu Arg Val Val
 125
 40 Arg Lys Val Arg Pro

(2) INFORMATION FOR SEQ ID NO:27:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1219 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid (Edited Contig 2692004)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:27:

60 GCACGCCGAC CGGCGCCGGG AGATCCTGGC AAAGTATCCA GAGATAAAGT CCTTGATGAA 60
 ACCTGATCCC AATTTGATAT GGATTATAAT TATGATGGTT CTCACCCAGT TGGGTGCATT 120
 TTACATAGTA AAAGACTTGG ACTGGAAATG GGTCAATTTT GGGGCCTATG CGTTTGGCAG 180
 TTGCATTAAAC CACTCAATGA CTCTGGCTAT TCATGAGATT GCCACAATG CTGCCTTTGG 240
 65 CAACTGCAAA GCAATGTGGA ATCGCTGGTT TGAATGTTT GCTAATCTTC CTATTGGGAT 300

5 TCCATATTCA ATTTCTTTA AGAGGTATCA CATGGATCAT CATCGGTACC TTGGAGCTGA 360
 TGGCGTCGAT GTAGATATTC CTACCGATTT TGAGGGCTGG TTCTTCTGTA CCGCTTTCAG 420
 AAAGTTTATA TGGGTTATTC TTCAGCCTCT CTTTTATGCC TTTCGACCTC TGTTTCATCAA 480
 10 CCCCCAACCA ATTACGTATC TGGAAGTTAT CAATACCGTG GCACAGGTCA CTTTTGACAT 540
 TTTAATTTAT TACTTTTTTG GAATTAAATC CTTAGTCTAC ATGTTGGCAG CATCTTTACT 600
 TGGCCTGGGT TTGCACCCAA TTTCTGGACA TTTTATAGCT GAGCATTACA TGTTCTTAAA 660
 15 GGGTCATGAA ACTTACTCAT ATTATGGGCC TCTGAATTTA CTTACCTTCA ATGTGGGTTA 720
 TCATAATGAA CATCATGATT TCCCCAACAT TCCTGGAAAA AGTCTTCCAC TGGTGAGGAA 780
 AATAGCAGCT GAATACTATG ACAACCTCCC TCACTACAAT TCCTGGATAA AAGTACTGTA 840
 20 TGATTTTGTG ATGGATGATA CAATAAGTCC CTAACAAGA ATGAAGAGGC ACCAAAAAGG 900
 AGAGATGGTG CTGGAGTAAA TATCATTAGT GCCAAAGGGA TTCTTCTCCA AAACCTTTAGA 960
 25 TGATAAAATG GAATTTTTGC ATTATTAAAC TTGAGACCAG TGATGCTCAG AAGCTCCCCT 1020
 GGCACAATTT CAGAGTAAGA GCTCGGTGAT ACCAAGAAGT GAATCTGGCT TTAAACAGT 1080
 CAGCCTGACT CTGTACTGCT CAGTTTCACT CACAGGAAAC TTGTGACTTG TGTATTATCG 1140
 30 TCATTGAGGA TGTTTCACTC ATGTCTGTCA TTTTATAAGC ATATCATTTA AAAAGCTTCT 1200
 AAAAAGCTAT TTCGCCAGG 1219

35 (2) INFORMATION FOR SEQ ID NO:28:

40 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 655 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid (Edited Contig 2153526)

45 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:28:

50 TTACCTTCTA CGTCCGCTTC TTCCTCACTT ATGTGCCACT ATTGGGGCTG AAAGCTTCCT 60
 GGGCCTTTTC TTCATAGTCA GGTTCCTGGA AAGCAACTGG TTTGTGTGGG TGACACAGAT 120
 GAACCATATT CCCATGCACA TTGATCATGA CCGGAACATG GACTGGGTTT CCACCCAGCT 180
 55 CCAGGCCACA TGCAATGTCC ACAAGTCTGC CTTCAATGAC TGGTTCAGTG GACACCTCAA 240
 CTTCCAGATT GAGCACCATC TTTTCCCAC GATGCCTCGA CACAATTACC ACAAAGTGGC 300
 60 TCCCCTGGTG CAGTCCTTGT GTGCCAAGCA TGGCATAGAG TACCAGTCCA AGCCCCTGCT 360
 GTCAGCCTTC GCCGACATCA TCCACTCACT AAAGGAGTCA GGGCAGCTCT GGCTAGATGC 420
 CTATCTTCAC CAATAACAAC AGCCACCCTG CCCAGTCTGG AAGAAGAGGA GGAAGACTCT 480
 65 GGAGCCAAGG CAGAGGGGAG CTTGAGGGAC AATGCCACTA TAGTTTAATA CTCAGAGGGG 540

GTTGGGTTTG GGGACATAAA GCCTCTGACT CAAACTCCTC CCTTTTATCT TCTAGCCACA 600
 GTTCTAAGAC CCAAAGTGGG GGGTGGACAC AGAAGTCCCT AGGAGGGAAG GAGCT 655

(2) INFORMATION FOR SEQ ID NO:29:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 304 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid (Edited Contig 3506132)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:29:

GTCTTTTACT TTGGCAATGG CTGGATTCCCT ACCCTCATCA CGGCCTTTGT CCTTGCTACC 60
 TCTCAGGCCC AAGCTGGATG GCTGCAACAT GATTATGGCC ACCTGTCTGT CTACAGAAAA 120
 CCCAAGTGGG ACCACCTTGT CCACAAATTC GTCATTGGCC ACTTAAAGGG TGCCTCTGCC 180
 AACTGGTGGG ATCATCGCCA CTTCCAGCAC CAGCCAAGC CTAACATCTT CCACAAGGAT 240
 CCCGATGTGA ACATGCTGCA CGTGTTTGTG CTGGGCGAAT GGCAGCCCAT CGAGTACGGC 300
 AAGA 304

(2) INFORMATION FOR SEQ ID NO:30:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 918 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid (Edited Contig 3854933)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:30:

CAGGGACCTA CCCCGCGCTA CTTACCTGG GACGAGGTGG CCCAGCGCTC AGGGTGCAGG 60
 GAGCGGTGGC TAGTGATCGA CCGTAAGGTG TACAACATCA GCGAGTTCAC CCGCCGGCAT 120
 CCAGGGGGCT CCCGGGTCAT CAGCCACTAC GCCGGGCAGG ATGCCACGGA TCCCTTTGTG 180
 GCCTTCCACA TCAACAAGGG CTTGTGAAG AAGTATATGA ACTCTCTCCT GATTGGAGAA 240
 CTGTCTCCAG AGCAGCCCAG CTTTGAGCCC ACCAAGAATA AAGAGCTGAC AGATGAGTTC 300
 CGGGAGCTGC GGGCCACAGT GGAGCGGATG GGGCTCATGA AGGCCAACCA TGTCTTCTTC 360
 CTGCTGTACC TGCTGCACAT CTTGCTGCTG GATGGTGCAG CCTGGCTCAC CTTTGGGTC 420
 TTTGGGACGT CCTTTTGGCC CTTCTCCTC TGTGCGGTGC TGCTCAGTGC AGTTCAGGCC 480
 CAGGCTGGCT GGCTGCAGCA TGACTTTGGG CACCTGTCGG TCTTCAGCAC CTCAAAGTGG 540
 AACCATCTGC TACATCATTT TGTGATTGGC CACCTGAAGG GGGCCCCCGC CAGTTGGTGG 600
 AACCACATGC ACTTCCAGCA CCATGCCAAG CCCAACTGCT TCCGCAAAGA CCCAGACATC 660

AACATGCATC CCTTCTTCTT TGCCTTGGGG AAGATCCTCT CTGTGGAGCT TGGGAAACAG 720
 AAGAAAAAAT ATATGCCGTA CAACCACCAG CACARATACT TCTTCCTAAT TGGGCCCCCA 780
 5 GCCTTGCTGC CTCTCTACTT CCAGTGGTAT ATTTTCTATT TTGTTATCCA GCGAAAGAAG 840
 TGGGTGGACT TGGCCTGGAT CAGCAAACAG GAATACGATG AAGCCGGGCT TCCATTGTCC 900
 10 ACCGCAAATG CTTCTAAA 918

(2) INFORMATION FOR SEQ ID NO:31:

- 15 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 1686 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear
 20 (ii) MOLECULE TYPE: other nucleic acid (Edited Contig 2511785)
 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:31:

25 GCCACTTAAA GGGTGCCTCT GCCAACTGGT GGAATCATCG CCACTTCCAG CACCACGCCA 60
 AGCCTAACAT CTTCCACAAG GATCCCGATG TGAACATGCT GCACGTGTTT GTTCTGGGCG 120
 30 AATGGCAGCC CATCGAGTAC GGCAAGAAGA AGCTGAAATA CCTGCCCTAC AATCACCAGC 180
 ACGAATACTT CTTCTGATT GGGCCGCCGC TGCTCATCCC CATGTATTTT CAGTACCAGA 240
 TCATCATGAC CATGATCGTC CATAAGAACT GGGTGGACCT GGCCTGGGCC GTCAGCTACT 300
 35 ACATCCGGTT CTTTCATCACC TACATCCCTT TCTACGGCAT CCTGGGAGCC CTCCTTTTCC 360
 TCAACTTCAT CAGGTTCTTG GAGAGCCACT GGTTTGTGTG GGTACACAG ATGAATCACA 420
 40 TCGTCATGGA GATTGACCAG GAGGCCTACC GTGACTGGTT CAGTAGCCAG CTGACAGCCA 480
 CCTGCAACGT GGAGCAGTCC TTCTTCAACG ACTGGTTCAG TGGACACCTT AACTTCCAGA 540
 TTGAGCACCA CCTCTTCCCC ACCATGCCCC GGCACAACTT ACACAAGATC GCCCCGCTGG 600
 45 TGAAGTCTCT ATGTGCCAAG CATGGCATTG AATACCAGGA GAAGCCGCTA CTGAGGGCCC 660
 TGCTGGACAT CATCAGGTCC CTGAAGAAGT CTGGGAAGCT GTGGCTGGAC GCCTACCTTC 720
 50 ACAAATGAAG CCACAGCCCC CGGGACACCG TGGGGAAGGG GTGCAGGTGG GGTGATGGCC 780
 AGAGGAATGA TGGGCTTTTG TTCTGAGGGG TGTCCGAGAG GCTGGTGTAT GCACTGCTCA 840
 CGGACCCCAT GTTGATCTT TCTCCCTTTC TCCTCTCCTT TTTCTCTTCA CATCTCCCCC 900
 55 ATAGCACCTT GCCCTCATGG GACCTGCCCT CCCTCAGCCG TCAGCCATCA GCCATGGCCC 960
 TCCCAGTGCC TCCTAGCCCC TTCTTCCAAG GAGCAGAGAG GTGGCCACCG GGGGTGGCTC 1020
 60 TGCTCTACCT CCACTCTCTG CCCCTAAAGA TGGGAGGAGA CCAGCGGTCC ATGGGTCTGG 1080
 CCTGTGAGTC TCCCCTTGCA GCCTGGTCAC TAGGCATCAC CCCCCTTTG GTTCTTCAGA 1140
 TGCTCTTGGG GTTCATAGGG GCAGGTCTTA GTCGGGCAGG GCCCCTGACC CTCCCGCCT 1200
 65 GGCTTCACTC TCCCTGACGG CTGCCATTGG TCCACCCTTT CATAGAGAGG CTTGCTTTGT 1260

5
10
15

TACAAAGCTC GGGTCTCCCT CCTGCAGCTC GGTAAAGTAC CCGAGGCCTC TCTTAAGATG 1320
TCCAGGGCCC CAGGCCCCGCG GGCACAGCCA GCCCAAACCT TGGGCCCTGG AAGAGTCCTC 1380
CACCCCATCA CTAGAGTGCT CTGACCCTGG GCTTTCACGG GCCCATTTCC ACCGCCTCCC 1440
CAACTTGAGC CTGTGACCTT GGGACCAAAG GGGGAGTCCC TCGTCTCTTG TGA CTCAGCA 1500
GAGGCAGTGG CCACGTTTCA GAGGGGGCCG GCTGGCCTGG AGGCTCAGCC CACCCTCCAG 1560
CTTTTCTCTA GGGTGTCTTG AGGTCCAAGA TTCTGGAGCA ATCTGACCCT TCTCCAAAGG 1620
CTCTGTTATC AGCTGGGCAG TGCCAGCCAA TCCCTGGCCA TTTGGCCCCA GGGGACGTGG 1680
GCCCTG 1686

20 (2) INFORMATION FOR SEQ ID NO:32:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 1843 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: other nucleic acid (Contig 2535)
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:32:

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GTCTTTTACT TTGGCAATGG CTGGATTCCT ACCCTCATCA CGGCCTTTGT CCTTGCTACC 60
TCTCAGGCCC AAGCTGGATG GCTGCAACAT GATTATGGCC ACCTGTCTGT CTACAGAAAA 120
CCCAAGTGGA ACCACCTTGT CCACAAATTC GTCATTGGCC ACTTAAAGGG TGCCTCTGCC 180
AACTGGTGGA ATCATCGCCA CTTCCAGCAC CACGCCAAGC CTAACATCTT CCACAAGGAT 240
CCCGATGTGA ACATGCTGCA CGTGTTTGTT CTGGGCGAAT GGCAGCCCAT CGAGTACGGC 300
AAGAAGAAGC TGAAATACCT GCCCTACAAT CACCAGCACG AATACTTCTT CCTGATTGGG 360
CCGCCGCTGC TCATCCCCAT GTATTTCCAG TACCAGATCA TCATGACCAT GATCGTCCAT 420
AAGAACTGGG TGGACCTGGC CTGGGCGGTC AGCTACTACA TCCGTTTCTT CATCACCTAC 480
ATCCCTTTCT ACGGCATCCT GGGAGCCCTC CTTTCTCTCA ACTTCATCAG GTTCCTGGAG 540
AGCCACTGGT TTGTGTGGGT CACACAGATG AATCACATCG TCATGGAGAT TGACCAGGAG 600
GCCTACCGTG ACTGGTTCAG TAGCCAGCTG ACAGCCACCT GCAACGTGGA GCAGTCCTTC 660
TTCAACGACT GGTTCACTGG ACACCTTAAC TTCCAGATTG AGCACCACCT CTTCCCCACC 720
ATGCCCCGGC ACAACTTACA CAAGATCGCC CCGCTGGTGA AGTCTCTATG TGCCAAGCAT 780
GGCATTGAAT ACCAGGAGAA GCCGCTACTG AGGGCCCTGC TGGACATCAT CAGGTCCCTG 840
AAGAAGTCTG GGAAGCTGTG GCTGGACGCC TACCTTCACA AATGAAGCCA CAGCCCCCGG 900
GACACCGTGG GGAAGGGGTG CAGGTGGGGT GATGGCCAGA GGAATGATGG GCTTTTGTTC 960
TGAGGGGTGT CCGAGAGGCT GGTGTATGCA CTGCTCACGG ACCCATGTT GGATCTTTCT 1020

CCCTTTCTCC TCTCCTTTTT CTCTTCACAT CTCCCCATA GCACCCTGCC CTCATGGGAC 1080
 CTGCCCTCCC TCAGCCGTCA GCCATCAGCC ATGGCCCTCC CAGTGCCCTCC TAGCCCCTTC 1140
 5 TTCCAAGGAG CAGAGAGGTG GCCACCGGGG GTGGCTCTGT CCTACCTCCA CTCTCTGCCC 1200
 CTAAAGATGG GAGGAGACCA GCGGTCCATG GGTCTGGCCT GTGAGTCTCC CTTGTCAGCC 1260
 10 TGGTCACTAG GCATCACCCC CGCTTTGGTT CTTCAGATGC TCTTGGGGTT CATAGGGGCA 1320
 GGTCCCTAGTC GGGCAGGGCC CCTGACCCTC CCGGCCTGGC TTCACTCTCC CTGACGGCTG 1380
 CCATTGGTCC ACCCTTTCAT AGAGAGGCCT GCTTTGTTAC AAAGCTCGGG TCTCCCTCCT 1440
 15 GCAGCTCGGT TAAGTACCCG AGGCCTCTCT TAAGATGTCC AGGGCCCCAG GCCCGCGGGC 1500
 ACAGCCAGCC CAAACCTTGG GCCCTGGAAG AGTCCTCCAC CCCATCACTA GAGTGCTCTG 1560
 20 ACCCTGGGCT TTCACGGGCC CCATTCCACC GCCTCCCCAA CTTGAGCCTG TGACCTTGGG 1620
 ACCAAAGGGG GAGTCCCTCG TCTCTTGTGA CTCAGCAGAG GCAGTGGCCA CGTTCAGGGA 1680
 GGGGCCGGCT GGCCTGGAGG CTCAGCCCAC CCTCCAGCTT TTCCTCAGGG TGTCTGAGG 1740
 25 TCCAAGATTC TGGAGCAATC TGACCCTTCT CCAAAGGCTC TGTTCATCAGC TGGGCAGTGC 1800
 CAGCCAATCC CTGGCCATTT GGCCCCAGGG GACGTGGGCC CTG 1843

30 (2) INFORMATION FOR SEQ ID NO:33:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 2257 base pairs
 (B) TYPE: nucleic acid
 35 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear
 (ii) MOLECULE TYPE: other nucleic acid (Edited Contig 253538a)
 40 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:33:

CAGGGACCTA CCCC GCGCTA CTTACCTGG GACGAGGTGG CCCAGCGCTC AGGGTGCGAG 60
 45 GAGCGGTGGC TAGTGATCGA CCGTAAGGTG TACAACATCA GCGAGTTCAC CCGCCGGCAT 120
 CCAGGGGGCT CCCGGGTCAT CAGCCACTAC GCCGGGCAGG ATGCCACGGA TCCCTTTGTG 180
 GCCTTCACA TCAACAAGGG CTTGTGAAG AAGTATATGA ACTCTCTCCT GATTGGAGAA 240
 50 CTGTCTCCAG AGCAGCCCAG CTTTGAGCCC ACCAAGAATA AAGAGCTGAC AGATGAGTTC 300
 CGGGAGCTGC GGGCCACAGT GGAGCGGATG GGGCTCATGA AGGCCAACCA TGTCTTCTTC 360
 55 CTGTGTACC TGCTGCACAT CTTGCTGCTG GATGGTGCAG CCTGGCTCAC CTTTGGGTC 420
 TTTGGGACGT CCTTTTGGC CTTCTCTC TGTGCGGTGC TGCTCAGTGC AGTTCAGCAG 480
 GCCCAGCTG GATGGCTGCA ACATGATTAT GGCCACCTGT CTGTCTACAG AAAACCCAAG 540
 60 TGGAACCACC TTGTCCACAA ATTCGTCATT GGCCACTTAA AGGGTGCCTC TGCCAACCTG 600
 TGGAATCATC GCCACTTCCA GCACCACGCC AAGCCTAACA TCTTCACAA GGATCCCGAT 660
 65 GTGAACATGC TGCACGTGTT TGTCTGGGC GAATGGCAGC CCATCGAGTA CGGCAAGAAG 720

AAGCTGAAAT ACCTGCCCTA CAATCACCAG CACGAATACT TCTTCCTGAT TGGGCCGCCG 780
 CTGCTCATCC CCATGTATTT CCAGTACCAG ATCATCATGA CCATGATCGT CCATAAGAAC 840
 5 TGGGTGGACC TGGCCTGGGC CGTCAGCTAC TACATCCGGT TCTTCATCAC CTACATCCCT 900
 TTCTACGGCA TCCTGGGAGC CCTCCTTTTC CTCAACTTCA TCAGGTTTCCT GGAGAGCCAC 960
 10 TGGTTTGTGT GGGTCACACA GATGAATCAC ATCGTCATGG AGATTGACCA GGAGGCCTAC 1020
 CGTGACTGGT TCAGTAGCCA GCTGACAGCC ACCTGCAACG TGGAGCAGTC CTTCTTCAAC 1080
 GACTGGTTCA GTGGACACCT TAACTTCCAG ATTGAGCACC ACCTCTTCCC CACCATGCCC 1140
 15 CGGCACAACT TACACAAGAT CGCCCCGCTG GTGAAGTCTC TATGTGCCAA GCATGGCATT 1200
 GAATACCAGG AGAAGCCGCT ACTGAGGGCC CTGCTGGACA TCATCAGGTC CCTGAAGAAG 1260
 20 TCTGGGAAGC TGTGGCTGGA CGCCTACCTT CACAAATGAA GCCACAGCCC CCGGGACACC 1320
 GTGGGGAAGG GGTGCAGGTG GGGTGATGGC CAGAGGAATG ATGGGCTTTT GTTCTGAGGG 1380
 GTGTCCGAGA GGCTGGTGTA TGCACTGCTC ACGGACCCCA TGTTCGATCT TTCTCCCTTT 1440
 25 CTCCTCTCCT TTTTCTCTTC ACATCTCCCC CATAGCAGCC TGCCCTCATG GGACCTGCCC 1500
 TCCCTCAGCC GTCAGCCATC AGCCATGGCC CTCCCAGTGC CTCCTAGCCC CTTCTTCCAA 1560
 30 GGAGCAGAGA GGTGGCCACC GGGGGTGGCT CTGTCCTACC TCCACTCTCT GCCCCTAAAG 1620
 ATGGGAGGAG ACCAGCGGTC CATGGGTCTG GCCTGTGAGT CTCCCCTTGC AGCCTGGTCA 1680
 CTAGGCATCA CCCCCGCTTT GGTTCCTCAG ATGCTCTTGG GGTTCATAGG GGCAGGTCCT 1740
 35 AGTCGGGCAG GGCCCCTGAC CCTCCCGGCC TGGCTTCACT CTCCTGACG GCTGCCATTG 1800
 GTCCACCCTT TCATAGAGAG GCCTGCTTTG TTACAAAGCT CGGGTCTCCC TCCTGCAGCT 1860
 40 CGGTTAAGTA CCCGAGGCCT CTCTTAAGAT GTCCAGGGCC CCAGGCCCGC GGGCACAGCC 1920
 AGCCCAAACC TTGGGCCCTG GAAGAGTCCT CCACCCCATC ACTAGAGTGC TCTGACCCTG 1980
 GGCTTTCACG GGCCCCATTC CACCGCCTCC CCAACTTGAG CCTGTGACCT TGGGACCAAA 2040
 45 GGGGGAGTCC CTCGTCTCTT GTGACTCAGC AGAGGCAGTG GCCACGTTCA GGGAGGGGCC 2100
 GGCTGGCCTG GAGGCTCAGC CCACCCTCCA GCTTTTCCTC AGGGTGTCTT GAGGTCCAAG 2160
 50 ATTCTGGAGC AATCTGACCC TTCTCAAAG GCTCTGTTAT CAGCTGGGCA GTGCCAGCCA 2220
 ATCCCTGGCC ATTTGGCCCC AGGGGACGTG GGCCCTG 2257

55 (2) INFORMATION FOR SEQ ID NO:34:
 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 411 amino acids
 (B) TYPE: amino acid
 60 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear
 (ii) MOLECULE TYPE: amino acid (Translation of Contig 2692004)
 65 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:34:

	His	Ala	Asp	Arg	Arg	Arg	Glu	Ile	Leu	Ala	Lys	Tyr	Pro	Glu	Ile	
	1				5					10					15	
5	Lys	Ser	Leu	Met	Lys	Pro	Asp	Pro	Asn	Leu	Ile	Trp	Ile	Ile	Ile	
					20					25					30	
	Met	Met	Val	Leu	Thr	Gln	Leu	Gly	Ala	Phe	Tyr	Ile	Val	Lys	Asp	
					35					40					45	
	Leu	Asp	Trp	Lys	Trp	Val	Ile	Phe	Gly	Ala	Tyr	Ala	Phe	Gly	Ser	
					50					55					60	
10	Cys	Ile	Asn	His	Ser	Met	Thr	Leu	Ala	Ile	His	Glu	Ile	Ala	His	
					65					70					75	
	Asn	Ala	Ala	Phe	Gly	Asn	Cys	Lys	Ala	Met	Trp	Asn	Arg	Trp	Phe	
					80					85					90	
15	Gly	Met	Phe	Ala	Asn	Leu	Pro	Ile	Gly	Ile	Pro	Tyr	Ser	Ile	Ser	
					95					100					105	
	Phe	Lys	Arg	Tyr	His	Met	Asp	His	His	Arg	Tyr	Leu	Gly	Ala	Asp	
					110					115					120	
	Gly	Val	Asp	Val	Asp	Ile	Pro	Thr	Asp	Phe	Glu	Gly	Trp	Phe	Phe	
					125					130					135	
20	Cys	Thr	Ala	Phe	Arg	Lys	Phe	Ile	Trp	Val	Ile	Leu	Gln	Pro	Leu	
					140					145					150	
	Phe	Tyr	Ala	Phe	Arg	Pro	Leu	Phe	Ile	Asn	Pro	Lys	Pro	Ile	Thr	
					155					160					165	
25	Tyr	Leu	Glu	Val	Ile	Asn	Thr	Val	Ala	Gln	Val	Thr	Phe	Asp	Ile	
					170					175					180	
	Leu	Ile	Tyr	Tyr	Phe	Leu	Gly	Ile	Lys	Ser	Leu	Val	Tyr	Met	Leu	
					185					190					195	
	Ala	Ala	Ser	Leu	Leu	Gly	Leu	Gly	Leu	His	Pro	Ile	Ser	Gly	His	
					200					205					210	
30	Phe	Ile	Ala	Glu	His	Tyr	Met	Phe	Leu	Lys	Gly	His	Glu	Thr	Tyr	
					215					220					225	
	Ser	Tyr	Tyr	Gly	Pro	Leu	Asn	Leu	Leu	Thr	Phe	Asn	Val	Gly	Tyr	
					230					235					240	
35	His	Asn	Glu	His	His	Asp	Phe	Pro	Asn	Ile	Pro	Gly	Lys	Ser	Leu	
					245					250					255	
	Pro	Leu	Val	Arg	Lys	Ile	Ala	Ala	Glu	Tyr	Tyr	Asp	Asn	Leu	Pro	
					260					265					270	
	His	Tyr	Asn	Ser	Trp	Ile	Lys	Val	Leu	Tyr	Asp	Phe	Val	Met	Asp	
					275					280					285	
40	Asp	Thr	Ile	Ser	Pro	Tyr	Ser	Arg	Met	Lys	Arg	His	Gln	Lys	Gly	
					290					295					300	
	Glu	Met	Val	Leu	Glu	Xaa	Ile	Ser	Leu	Val	Pro	Lys	Gly	Phe	Phe	
					305					310					315	
45	Ser	Lys	Thr	Leu	Asp	Asp	Lys	Met	Glu	Phe	Leu	His	Tyr	Xaa	Thr	
					320					325					330	
	Xaa	Asp	Gln	Xaa	Cys	Ser	Glu	Ala	Pro	Leu	Ala	Gln	Phe	Gln	Ser	
					335					340					345	
	Lys	Ser	Ser	Val	Ile	Pro	Arg	Ser	Glu	Ser	Gly	Phe	Xaa	Thr	Val	
					350					355					360	
50	Ser	Leu	Thr	Leu	Tyr	Cys	Ser	Val	Ser	Leu	Thr	Gly	Asn	Leu	Xaa	
					365					370					375	
	Leu	Val	Tyr	Tyr	Arg	His	Xaa	Gly	Cys	Phe	Thr	His	Val	Cys	His	
					380					385					390	
55	Phe	Ile	Ser	Ile	Ser	Phe	Lys	Lys	Leu	Leu	Lys	Ser	Tyr	Phe	Ala	
					400					405					410	
	Arg															

(2) INFORMATION FOR SEQ ID NO:35:

- 60 (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 218 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - 65 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: amino acid (Translation of Contig 2153526)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:35:

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Tyr Leu Leu Arg Pro Leu Leu Pro His Leu Cys Ala Thr Ile Gly
1 5 10 15
Ala Glu Ser Phe Leu Gly Leu Phe Phe Ile Val Arg Phe Leu Glu
20 25 30
Ser Asn Trp Phe Val Trp Val Thr Gln Met Asn His Ile Pro Met
35 40 45
His Ile Asp His Asp Arg Asn Met Asp Trp Val Ser Thr Gln Leu
50 55 60
Gln Ala Thr Cys Asn Val His Lys Ser Ala Phe Asn Asp Trp Phe
65 70 75
Ser Gly His Leu Asn Phe Gln Ile Glu His His Leu Phe Pro Thr
80 85 90
Met Pro Arg His Asn Tyr His Lys Val Ala Pro Leu Val Gln Ser
95 100 105
Leu Cys Ala Lys His Gly Ile Glu Tyr Gln Ser Lys Pro Leu Leu
110 115 120
Ser Ala Phe Ala Asp Ile Ile His Ser Leu Lys Glu Ser Gly Gln
125 130 135
Leu Trp Leu Asp Ala Tyr Leu His Gln Xaa Gln Gln Pro Pro Cys
140 145 150
Pro Val Trp Lys Lys Arg Arg Lys Thr Leu Glu Pro Arg Gln Arg
155 160 165
Gly Ala Xaa Gly Thr Met Pro Leu Xaa Phe Asn Thr Gln Arg Gly
170 175 180
Leu Gly Leu Gly Thr Xaa Ser Leu Xaa Leu Lys Leu Leu Pro Phe
185 190 195
Ile Phe Xaa Pro Gln Phe Xaa Asp Pro Lys Trp Gly Val Asp Thr
200 205 210
Glu Val Pro Arg Arg Glu Gly Ala
215

(2) INFORMATION FOR SEQ ID NO:36:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 86 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: amino acid (Translation of Contig 3506132)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:36:

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Val Phe Tyr Phe Gly Asn Gly Trp Ile Pro Thr Leu Ile Thr Ala
1 5 10 15
Phe Val Leu Ala Thr Ser Gln Ala Gln Ala Gly Trp Leu Gln His
20 25 30
Asp Tyr Gly His Leu Ser Val Tyr Arg Lys Pro Lys Trp Asn His
35 40 45
Leu Val His Lys Phe Val Ile Gly His Leu Lys Gly Ala Ser Ala
50 55 60
Asn Trp Trp Asn His Arg His Phe Gln His His Ala Lys Pro Asn
65 70 75
Leu Gly Glu Trp Gln Pro Ile Glu Tyr Gly Lys Xaa
80 85

(2) INFORMATION FOR SEQ ID NO:37:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 306 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: amino acid (Translation of Contig 3854933)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:37:

Gln	Gly	Pro	Thr	Pro	Arg	Tyr	Phe	Thr	Trp	Asp	Glu	Val	Ala	Gln
1				5					10					15
Arg	Ser	Gly	Cys	Glu	Glu	Arg	Trp	Leu	Val	Ile	Asp	Arg	Lys	Val
				20					25					30
Tyr	Asn	Ile	Ser	Glu	Phe	Thr	Arg	Arg	His	Pro	Gly	Gly	Ser	Arg
				35					40					45
Val	Ile	Ser	His	Tyr	Ala	Gly	Gln	Asp	Ala	Thr	Asp	Pro	Phe	Val
				50					55					60
Ala	Phe	His	Ile	Asn	Lys	Gly	Leu	Val	Lys	Lys	Tyr	Met	Asn	Ser
				65					70					75
Leu	Leu	Ile	Gly	Glu	Leu	Ser	Pro	Glu	Gln	Pro	Ser	Phe	Glu	Pro
				80					85					90
Thr	Lys	Asn	Lys	Glu	Leu	Thr	Asp	Glu	Phe	Arg	Glu	Leu	Arg	Ala
				95					100					105
Thr	Val	Glu	Arg	Met	Gly	Leu	Met	Lys	Ala	Asn	His	Val	Phe	Phe
				110					115					120
Leu	Leu	Tyr	Leu	Leu	His	Ile	Leu	Leu	Leu	Asp	Gly	Ala	Ala	Trp
				125					130					135
Leu	Thr	Leu	Trp	Val	Phe	Gly	Thr	Ser	Phe	Leu	Pro	Phe	Leu	Leu
				140					145					150
Cys	Ala	Val	Leu	Leu	Ser	Ala	Val	Gln	Ala	Gln	Ala	Gly	Trp	Leu
				155					160					165
Gln	His	Asp	Phe	Gly	His	Leu	Ser	Val	Phe	Ser	Thr	Ser	Lys	Trp
				170					175					180
Asn	His	Leu	Leu	His	His	Phe	Val	Ile	Gly	His	Leu	Lys	Gly	Ala
				185					190					195
Pro	Ala	Ser	Trp	Trp	Asn	His	Met	His	Phe	Gln	His	His	Ala	Lys
				200					205					210
Pro	Asn	Cys	Phe	Arg	Lys	Asp	Pro	Asp	Ile	Asn	Met	His	Pro	Phe
				215					220					225
Phe	Phe	Ala	Leu	Gly	Lys	Ile	Leu	Ser	Val	Glu	Leu	Gly	Lys	Gln
				230					235					240
Lys	Lys	Lys	Tyr	Met	Pro	Tyr	Asn	His	Gln	His	Xaa	Tyr	Phe	Phe
				245					250					255
Leu	Ile	Gly	Pro	Pro	Ala	Leu	Leu	Pro	Leu	Tyr	Phe	Gln	Trp	Tyr
				260					265					270
Ile	Phe	Tyr	Phe	Val	Ile	Gln	Arg	Lys	Lys	Trp	Val	Asp	Leu	Ala
				275					280					285
Trp	Ile	Ser	Lys	Gln	Glu	Tyr	Asp	Glu	Ala	Gly	Leu	Pro	Leu	Ser
				290					295					300
Thr	Ala	Asn	Ala	Ser	Lys									305

(2) INFORMATION FOR SEQ ID NO:38:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 566 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: amino acid (Translation of Contig 2511785)

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO:38:

	His	Leu	Lys	Gly	Ala	Ser	Ala	Asn	Trp	Trp	Asn	His	Arg	His	Phe	
	1				5					10					15	
10	Gln	His	His	Ala	Lys	Pro	Asn	Ile	Phe	His	Lys	Asp	Pro	Asp	Val	
					20					25					30	
	Asn	Met	Leu	His	Val	Phe	Val	Leu	Gly	Glu	Trp	Gln	Pro	Ile	Glu	
					35					40					45	
15	Tyr	Gly	Lys	Lys	Lys	Leu	Lys	Tyr	Leu	Pro	Tyr	Asn	His	Gln	His	
					50					55					60	
	Glu	Tyr	Phe	Phe	Leu	Ile	Gly	Pro	Pro	Leu	Leu	Ile	Pro	Met	Tyr	
					65					70					75	
	Phe	Gln	Tyr	Gln	Ile	Ile	Met	Thr	Met	Ile	Val	His	Lys	Asn	Trp	
					80					85					90	
20	Val	Asp	Leu	Ala	Trp	Ala	Val	Ser	Tyr	Tyr	Ile	Arg	Phe	Phe	Ile	
					95					100					105	
	Thr	Tyr	Ile	Pro	Phe	Tyr	Gly	Ile	Leu	Gly	Ala	Leu	Leu	Phe	Leu	
					110					115					120	
25	Asn	Phe	Ile	Arg	Phe	Leu	Glu	Ser	His	Trp	Phe	Val	Trp	Val	Thr	
					125					130					135	
	Gln	Met	Asn	His	Ile	Val	Met	Glu	Ile	Asp	Gln	Glu	Ala	Tyr	Arg	
					140					145					150	
	Asp	Trp	Phe	Ser	Ser	Gln	Leu	Thr	Ala	Thr	Cys	Asn	Val	Glu	Gln	
					155					160					165	
30	Ser	Phe	Phe	Asn	Asp	Trp	Phe	Ser	Gly	His	Leu	Asn	Phe	Gln	Ile	
					170					175					180	
	Glu	His	His	Leu	Phe	Pro	Thr	Met	Pro	Arg	His	Asn	Leu	His	Lys	
					185					190					195	
35	Ile	Ala	Pro	Leu	Val	Lys	Ser	Leu	Cys	Ala	Lys	His	Gly	Ile	Glu	
					200					205					210	
	Tyr	Gln	Glu	Lys	Pro	Leu	Leu	Arg	Ala	Leu	Leu	Asp	Ile	Ile	Arg	
					215					220					225	
	Ser	Leu	Lys	Lys	Ser	Gly	Lys	Leu	Trp	Leu	Asp	Ala	Tyr	Leu	His	
					230					235					240	
40	Lys	Xaa	Ser	His	Ser	Pro	Arg	Asp	Thr	Val	Gly	Lys	Gly	Cys	Arg	
					245					250					255	
	Trp	Gly	Asp	Gly	Gln	Arg	Asn	Asp	Gly	Leu	Leu	Phe	Xaa	Gly	Val	
					260					265					270	
45	Ser	Glu	Arg	Leu	Val	Tyr	Ala	Leu	Leu	Thr	Asp	Pro	Met	Leu	Asp	
					275					280					285	
	Leu	Ser	Pro	Phe	Leu	Leu	Ser	Phe	Phe	Ser	Ser	His	Leu	Pro	His	
					290					295					300	
	Ser	Thr	Leu	Pro	Ser	Trp	Asp	Leu	Pro	Ser	Leu	Ser	Arg	Gln	Pro	
					305					310					315	
50	Ser	Ala	Met	Ala	Leu	Pro	Val	Pro	Pro	Ser	Pro	Phe	Phe	Gln	Gly	
					320					325					330	
	Ala	Glu	Arg	Trp	Pro	Pro	Gly	Val	Ala	Leu	Ser	Tyr	Leu	His	Ser	
					335					340					345	
55	Leu	Pro	Leu	Lys	Met	Gly	Gly	Asp	Gln	Arg	Ser	Met	Gly	Leu	Ala	
					350					355					360	
	Cys	Glu	Ser	Pro	Leu	Ala	Ala	Trp	Ser	Leu	Gly	Ile	Thr	Pro	Ala	
					365					370					375	
	Leu	Val	Leu	Gln	Met	Leu	Leu	Gly	Phe	Ile	Gly	Ala	Gly	Pro	Ser	
					380					385					390	
60	Arg	Ala	Gly	Pro	Leu	Thr	Leu	Pro	Ala	Trp	Leu	His	Ser	Pro	Xaa	
					400					405					410	
	Arg	Leu	Pro	Leu	Val	His	Pro	Phe	Ile	Glu	Arg	Pro	Ala	Leu	Leu	
					415					420					425	
65	Gln	Ser	Ser	Gly	Leu	Pro	Pro	Ala	Ala	Arg	Leu	Ser	Thr	Arg	Gly	
					430					435					440	

5 Leu Ser Xaa Asp Val Gln Gly Pro Arg Pro Ala Gly Thr Ala Ser
 445 450 455
 Pro Asn Leu Gly Pro Trp Lys Ser Pro Pro Pro His His Xaa Ser
 460 465 470
 10 Ala Leu Thr Leu Gly Phe His Gly Pro His Ser Thr Ala Ser Pro
 475 480 485
 Thr Xaa Ala Cys Asp Leu Gly Thr Lys Gly Gly Val Pro Arg Leu
 490 495 500
 Leu Xaa Leu Ser Arg Gly Ser Gly His Val Gln Gly Gly Ala Gly
 505 510 515
 Trp Pro Gly Gly Ser Ala His Pro Pro Ala Phe Pro Gln Gly Val
 520 525 530
 15 Leu Arg Ser Lys Ile Leu Glu Gln Ser Asp Pro Ser Pro Lys Ala
 535 540 545
 Leu Leu Ser Ala Gly Gln Cys Gln Pro Ile Pro Gly His Leu Ala
 550 555 560
 Pro Gly Asp Val Gly Pro Xaa
 565

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(2) INFORMATION FOR SEQ ID NO:39:

25 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 619 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

30 (ii) MOLECULE TYPE: amino acid (Translation of Contig 2535)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:39:

35 Val Phe Tyr Phe Gly Asn Gly Trp Ile Pro Thr Leu Ile Thr Ala
 1 5 10 15
 Phe Val Leu Ala Thr Ser Gln Ala Gln Ala Gly Trp Leu Gln His
 20 25 30
 40 Asp Tyr Gly His Leu Ser Val Tyr Arg Lys Pro Lys Trp Asn His
 35 40 45
 Leu Val His Lys Phe Val Ile Gly His Leu Lys Gly Ala Ser Ala
 50 55 60
 Asn Trp Trp Asn His Arg His Phe Gln His His Ala Lys Pro Asn
 65 70 75
 45 Ile Phe His Lys Asp Pro Asp Val Asn Met Leu His Val Phe Val
 80 85 90
 Leu Gly Glu Trp Gln Pro Ile Glu Tyr Gly Lys Lys Lys Leu Lys
 95 100 105
 50 Tyr Leu Pro Tyr Asn His Gln His Glu Tyr Phe Phe Leu Ile Gly
 110 115 120
 Pro Pro Leu Leu Ile Pro Met Tyr Phe Gln Tyr Gln Ile Ile Met
 125 130 135
 Thr Met Ile Val His Lys Asn Trp Val Asp Leu Ala Trp Ala Val
 140 145 150
 55 Ser Tyr Tyr Ile Arg Phe Phe Ile Thr Tyr Ile Pro Phe Tyr Gly
 155 160 165
 Ile Leu Gly Ala Leu Leu Phe Leu Asn Phe Ile Arg Phe Leu Glu
 170 175 180
 Ser His Trp Phe Val Trp Val Thr Gln Met Asn His Ile Val Met
 185 190 195
 60 Glu Ile Asp Gln Glu Ala Tyr Arg Asp Trp Phe Ser Ser Gln Leu
 200 205 210
 Thr Ala Thr Cys Asn Val Glu Gln Ser Phe Phe Asn Asp Trp Phe
 215 220 225
 65 Ser Gly His Leu Asn Phe Gln Ile Glu His His Leu Phe Pro Thr

		230		235		240
	Met Pro Arg His	Asn Leu His Lys Ile	Ala Pro Leu Val Lys Ser			
		245		250		255
5	Leu Cys Ala Lys	His Gly Ile Glu Tyr	Gln Glu Lys Pro Leu Leu			
		260		265		270
	Arg Ala Leu Leu	Asp Ile Ile Arg Ser	Leu Lys Lys Ser Gly Lys			
		275		280		285
	Leu Trp Leu Asp	Ala Tyr Leu His Lys	Xaa Ser His Ser Pro Arg			
		290		295		300
10	Asp Thr Val Gly	Lys Gly Cys Arg Trp	Gly Asp Gly Gln Arg Asn			
		305		310		315
	Asp Gly Leu Leu	Phe Xaa Gly Val Ser	Glu Arg Leu Val Tyr Ala			
		320		325		330
	Leu Leu Thr Asp	Pro Met Leu Asp Leu	Ser Pro Phe Leu Leu Ser			
15		335		340		345
	Phe Phe Ser Ser	His Leu Pro His Ser	Thr Leu Pro Ser Trp Asp			
		350		355		360
	Leu Pro Ser Leu	Ser Arg Gln Pro Ser	Ala Met Ala Leu Pro Val			
		365		370		375
20	Pro Pro Ser Pro	Phe Phe Gln Gly Ala	Glu Arg Trp Pro Pro Gly			
		380		385		390
	Val Ala Leu Ser	Tyr Leu His Ser Leu	Pro Leu Lys Met Gly Gly			
		400		405		410
	Asp Gln Arg Ser	Met Gly Leu Ala Cys	Glu Ser Pro Leu Ala Ala			
25		415		420		425
	Trp Ser Leu Gly	Ile Thr Pro Ala Leu	Val Leu Gln Met Leu Leu			
		430		435		440
	Gly Phe Ile Gly	Ala Gly Pro Ser Arg	Ala Gly Pro Leu Thr Leu			
		445		450		455
30	Pro Ala Trp Leu	His Ser Pro Xaa Arg	Leu Pro Leu Val His Pro			
		460		465		470
	Phe Ile Glu Arg	Pro Ala Leu Leu Gln	Ser Ser Gly Leu Pro Pro			
		475		480		485
	Ala Ala Arg Leu	Ser Thr Arg Gly Leu	Ser Xaa Asp Val Gln Gly			
35		490		495		500
	Pro Arg Pro Ala	Gly Thr Ala Ser Pro	Asn Leu Gly Pro Trp Lys			
		505		510		515
	Ser Pro Pro Pro	His His Xaa Ser Ala	Leu Thr Leu Gly Phe His			
		520		525		530
40	Gly Pro His Ser	Thr Ala Ser Pro Thr	Xaa Ala Cys Asp Leu Gly			
		535		540		545
	Thr Lys Gly Gly	Val Pro Arg Leu Leu	Xaa Leu Ser Arg Gly Ser			
		550		555		560
	Gly His Val Gln	Gly Gly Ala Gly Trp	Pro Gly Gly Ser Ala His			
45		565		570		575
	Pro Pro Ala Phe	Pro Gln Gly Val Leu	Arg Ser Lys Ile Leu Glu			
		580		585		590
	Gln Ser Asp Pro	Ser Pro Lys Ala Leu	Leu Ser Ala Gly Gln Cys			
		595		600		605
50	Gln Pro Ile Pro	Gly His Leu Ala Pro	Gly Asp Val Gly Pro Xaa			
		610		615		620

55

(2) INFORMATION FOR SEQ ID NO:40:

60

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 757 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

65

(ii) MOLECULE TYPE: amino acid (Translation of Contig 253538a)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:40:

	Gln	Gly	Pro	Thr	Pro	Arg	Tyr	Phe	Thr	Trp	Asp	Glu	Val	Ala	Gln
	1				5					10					15
5	Arg	Ser	Gly	Cys	Glu	Glu	Arg	Trp	Leu	Val	Ile	Asp	Arg	Lys	Val
					20					25					30
	Tyr	Asn	Ile	Ser	Glu	Phe	Thr	Arg	Arg	His	Pro	Gly	Gly	Ser	Arg
					35					40					45
10	Val	Ile	Ser	His	Tyr	Ala	Gly	Gln	Asp	Ala	Thr	Asp	Pro	Phe	Val
					50					55					60
	Ala	Phe	His	Ile	Asn	Lys	Gly	Leu	Val	Lys	Lys	Tyr	Met	Asn	Ser
					65					70					75
	Leu	Leu	Ile	Gly	Glu	Leu	Ser	Pro	Glu	Gln	Pro	Ser	Phe	Glu	Pro
					80					85					90
15	Thr	Lys	Asn	Lys	Glu	Leu	Thr	Asp	Glu	Phe	Arg	Glu	Leu	Arg	Ala
					95					100					105
	Thr	Val	Glu	Arg	Met	Gly	Leu	Met	Lys	Ala	Asn	His	Val	Phe	Phe
					110					115					120
20	Leu	Leu	Tyr	Leu	Leu	His	Ile	Leu	Leu	Leu	Asp	Gly	Ala	Ala	Trp
					125					130					135
	Leu	Thr	Leu	Trp	Val	Phe	Gly	Thr	Ser	Phe	Leu	Pro	Phe	Leu	Leu
					140					145					150
	Cys	Ala	Val	Leu	Leu	Ser	Ala	Val	Gln	Gln	Ala	Gln	Ala	Gly	Trp
					155					160					165
25	Leu	Gln	His	Asp	Tyr	Gly	His	Leu	Ser	Val	Tyr	Arg	Lys	Pro	Lys
					170					175					180
	Trp	Asn	His	Leu	Val	His	Lys	Phe	Val	Ile	Gly	His	Leu	Lys	Gly
					185					190					195
30	Ala	Ser	Ala	Asn	Trp	Trp	Asn	His	Arg	His	Phe	Gln	His	His	Ala
					200					205					210
	Lys	Pro	Asn	Ile	Phe	His	Lys	Asp	Pro	Asp	Val	Asn	Met	Leu	His
					215					220					225
	Val	Phe	Val	Leu	Gly	Glu	Trp	Gln	Pro	Ile	Glu	Tyr	Gly	Lys	Lys
					230					235					240
35	Lys	Leu	Lys	Tyr	Leu	Pro	Tyr	Asn	His	Gln	His	Glu	Tyr	Phe	Phe
					245					250					255
	Leu	Ile	Gly	Pro	Pro	Leu	Leu	Ile	Pro	Met	Tyr	Phe	Gln	Tyr	Gln
					260					265					270
40	Ile	Ile	Met	Thr	Met	Ile	Val	His	Lys	Asn	Trp	Val	Asp	Leu	Ala
					275					280					285
	Trp	Ala	Val	Ser	Tyr	Tyr	Ile	Arg	Phe	Phe	Ile	Thr	Tyr	Ile	Pro
					290					295					300
	Phe	Tyr	Gly	Ile	Leu	Gly	Ala	Leu	Leu	Phe	Leu	Asn	Phe	Ile	Arg
					305					310					315
45	Phe	Leu	Glu	Ser	His	Trp	Phe	Val	Trp	Val	Thr	Gln	Met	Asn	His
					320					325					330
	Ile	Val	Met	Glu	Ile	Asp	Gln	Glu	Ala	Tyr	Arg	Asp	Trp	Phe	Ser
					335					340					345
50	Ser	Gln	Leu	Thr	Ala	Thr	Cys	Asn	Val	Glu	Gln	Ser	Phe	Phe	Asn
					350					355					360
	Asp	Trp	Phe	Ser	Gly	His	Leu	Asn	Phe	Gln	Ile	Glu	His	His	Leu
					365					370					375
	Phe	Pro	Thr	Met	Pro	Arg	His	Asn	Leu	His	Lys	Ile	Ala	Pro	Leu
					380					385					390
55	Val	Lys	Ser	Leu	Cys	Ala	Lys	His	Gly	Ile	Glu	Tyr	Gln	Glu	Lys
					400					405					410
	Pro	Leu	Leu	Arg	Ala	Leu	Leu	Asp	Ile	Ile	Arg	Ser	Leu	Lys	Lys
					415					420					425
60	Ser	Gly	Lys	Leu	Trp	Leu	Asp	Ala	Tyr	Leu	His	Lys	Xaa	Ser	His
					430					435					440
	Ser	Pro	Arg	Asp	Thr	Val	Gly	Lys	Gly	Cys	Arg	Trp	Gly	Asp	Gly
					445					450					455
	Gln	Arg	Asn	Asp	Gly	Leu	Leu	Phe	Xaa	Gly	Val	Ser	Glu	Arg	Leu
					460					465					470
65	Val	Tyr	Ala	Leu	Leu	Thr	Asp	Pro	Met	Leu	Asp	Leu	Ser	Pro	Phe

			475			480		485
	Leu	Leu	Ser	Phe	Phe	Ser	Ser	His
						Leu	Pro	His
						Ser	Ser	Thr
						Leu	Pro	
5								
	Ser	Trp	Asp	Leu	Pro	Ser	Leu	Ser
						Arg	Gln	Pro
						Ser	Ala	Met
								Ala
	Leu	Pro	Val	Pro	Pro	Ser	Pro	Phe
						Phe	Gln	Gly
							Ala	Glu
							Arg	Trp
	Pro	Pro	Gly	Val	Ala	Leu	Ser	Tyr
						Leu	His	Ser
							Leu	Pro
							Leu	Lys
10								
	Met	Gly	Gly	Asp	Gln	Arg	Ser	Met
						Gly	Leu	Ala
							Cys	Glu
							Ser	Pro
	Leu	Ala	Ala	Trp	Ser	Leu	Gly	Ile
						Thr	Pro	Ala
							Leu	Val
							Leu	Gln
15								
	Met	Leu	Leu	Gly	Phe	Ile	Gly	Ala
						Gly	Pro	Ser
							Arg	Ala
							Gly	Pro
	Leu	Thr	Leu	Pro	Ala	Trp	Leu	His
						Ser	Pro	Xaa
							Arg	Leu
							Pro	Leu
	Val	His	Pro	Phe	Ile	Glu	Arg	Pro
						Ala	Leu	Gln
							Ser	Ser
							Gly	
20								
	Leu	Pro	Pro	Ala	Ala	Arg	Leu	Ser
						Thr	Arg	Gly
							Leu	Ser
							Xaa	Asp
	Val	Gln	Gly	Pro	Arg	Pro	Ala	Gly
						Thr	Ala	Ser
							Pro	Asn
							Leu	Gly
25								
	Pro	Trp	Lys	Ser	Pro	Pro	Pro	His
						His	Xaa	Ser
							Ala	Leu
							Thr	Leu
	Gly	Phe	His	Gly	Pro	His	Ser	Thr
						Ala	Ser	Pro
							Thr	Xaa
							Ala	Cys
	Asp	Leu	Gly	Thr	Lys	Gly	Gly	Val
						Pro	Arg	Leu
							Leu	Xaa
							Leu	Ser
30								
	Arg	Gly	Ser	Gly	His	Val	Gln	Gly
						Gly	Gly	Ala
							Gly	Trp
							Pro	Gly
	Ser	Ala	His	Pro	Pro	Ala	Phe	Pro
						Gln	Gly	Val
							Leu	Arg
							Ser	Lys
35								
	Ile	Leu	Glu	Gln	Ser	Asp	Pro	Ser
						Pro	Lys	Ala
							Leu	Leu
							Ser	Ala
	Gly	Gln	Cys	Gln	Pro	Ile	Pro	Gly
						His	Leu	Ala
							Pro	Gly
							Asp	Val
	Gly	Pro	Xaa					

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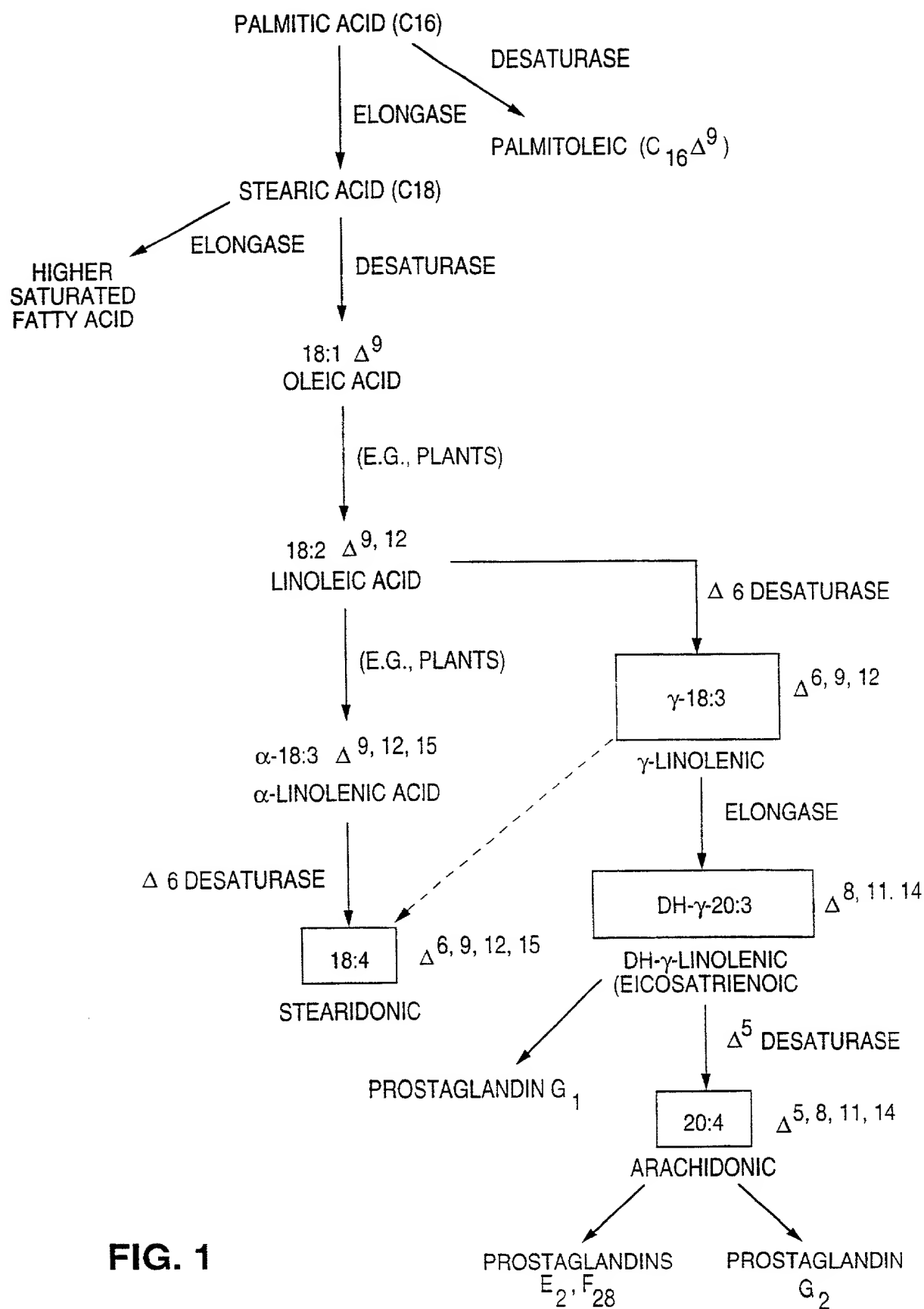


FIG. 1

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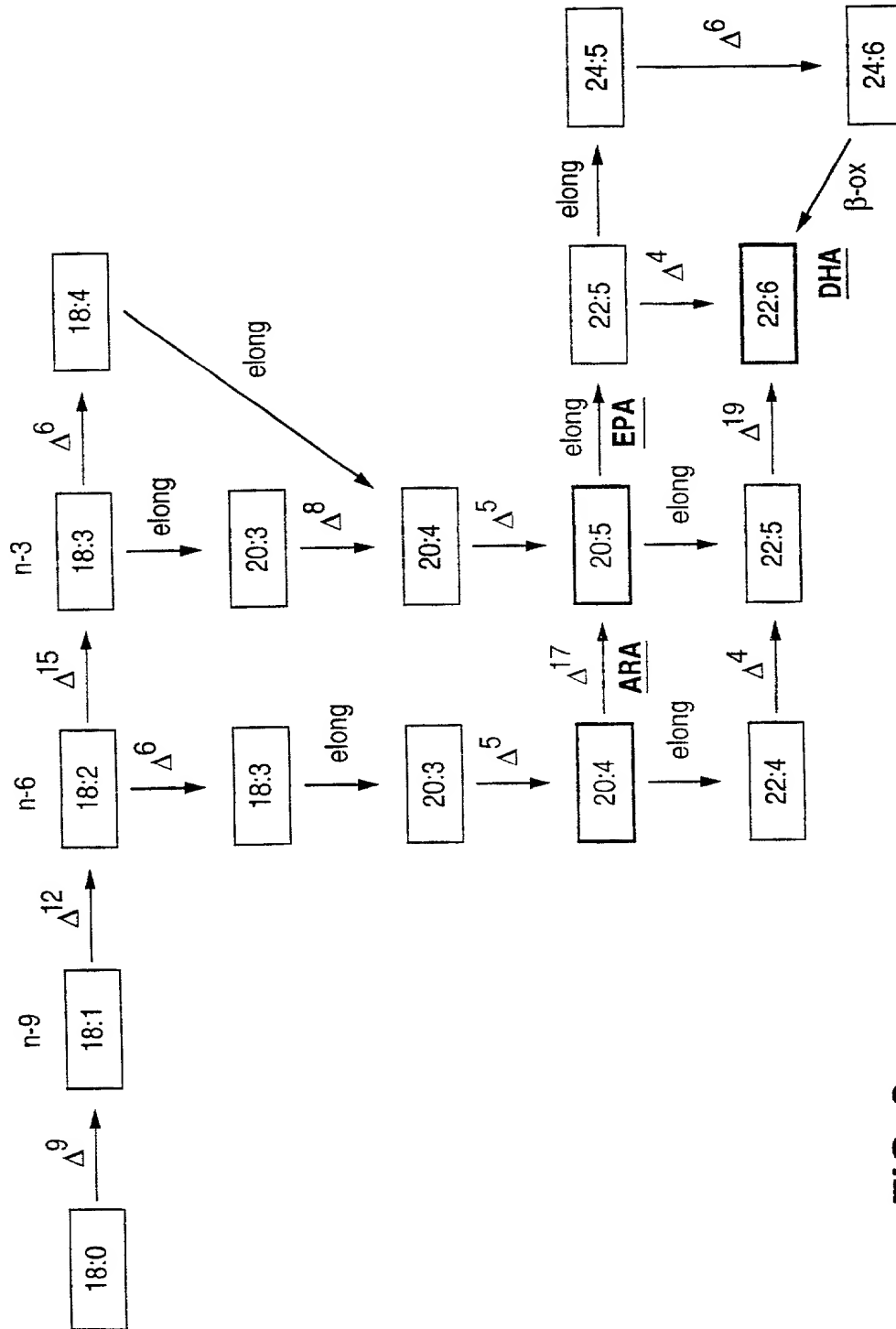


FIG. 2

60
 CGACACTCCT TCCTTCTTCT CACCCGTCCT AGTCCCCTTC AACCCCCCTC TTTGACAAAG
 ACAACAAACC ATG GCT GCT GCT CCC AGT GTG AGG ACG TTT ACT CGG GCC GAG
 Met Ala Ala Ala Pro Ser Val Arg Thr Phe Thr Arg Ala Glu
 120
 GTT TTG AAT GCC GAG GCT CTG AAT GAG GGC AAG GAT GCC GAG GCA
 Val Leu Asn Ala Glu Ala Leu Asn Glu Gly Lys Lys Asp Ala Glu Ala
 180
 CCC TTC TTG ATG ATC ATC GAC AAC AAG GTG TAC GAT GTC CGC GAG TTC
 Pro Phe Leu Met Ile Ile Asp Asn Lys Val Tyr Asp Val Arg Glu Phe
 240
 GTC CCT GAT CAT CCC GGT GGA AGT GTG ATT CTC ACG CAC GTT GGC AAG
 Val Pro Asp His Pro Gly Gly Ser Val Ile Leu Thr His Val Gly Lys
 300
 GAC GGC ACT GAC GTC TTT GAC ACT TTT CAC CCC GAG GCT GCT TGG GAG
 Asp Gly Thr Asp Val Phe Asp Thr Phe His Pro Glu Ala Ala Trp Glu
 360
 ACT CTT GCC AAC TTT TAC GTT GGT GAT ATT GAC GAG AGC GAC CGC GAT
 Thr Leu Ala Asn Phe Tyr Val Gly Asp Ile Asp Glu Ser Asp Arg Asp
 ATC AAG AAT GAT GAC TTT GCG GCC GAG GTC CGC AAG CTG CGT ACC TTG
 Ile Lys Asn Asp Phe Ala Ala Glu Val Arg Lys Leu Arg Thr Leu

FIG. 3A

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TTC Phe	CAG Gln	TCT Ser	CTT Leu	GGT Gly	TAC Tyr	TAC Tyr	GAT Asp	TCT Ser	TCC Ser	AAG Lys	GCA Ala	TAC Tyr	TAC Tyr	GCC Ala	TTC Phe
420 *															
AAG Lys	GTC Val	TCG Ser	TTC Phe	AAC Asn	CTC Leu	TGC Cys	ATC Ile	TGG Trp	GGT Gly	TTG Leu	TCG Ser	ACG Thr	GTC Val	ATT Ile	GTG Val
480 *															
GCC Ala	AAG Lys	TGG Trp	GGC Gly	CAG Gln	ACC Thr	TCG Ser	ACC Thr	CTC Leu	GCC Ala	AAC Asn	GTG Val	CTC Leu	TCG Ser	GCT Ala	GCG Ala
540 *															
CTT Leu	TTG Leu	GGT Gly	CTG Leu	TTC Phe	TGG Trp	CAG Gln	CAG Gln	TGC Cys	GGA Gly	TGG Trp	TTG Leu	GCT Ala	CAC His	GAC Asp	TTT Phe
600 *															
TTG Leu	CAT His	CAC His	CAG Gln	GTC Val	TTC Phe	CAG Gln	GAC Asp	CGT Arg	TTC Phe	TGG Trp	GGT Gly	GAT Asp	CTT Leu	TTC Phe	GGC Gly
660 *															
GCC Ala	TTC Phe	TTG Leu	GGA Gly	GGT Gly	GTC Val	TGC Cys	CAG Gln	GGC Gly	TTC Phe	TCG Ser	TCC Ser	TCG Ser	TGG Trp	TGG Trp	AAG Lys
720 *															
GAC Asp	AAG Lys	CAC His	AAC Asn	ACT Thr	CAC His	CAC His	GCC Ala	GCC Ala	CCC Pro	AAC Asn	GTC Val	CAC His	GGC Gly	GAG Glu	GAT Asp
780 *															

FIG. 3B

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CCC GAC ATT GAC ACC CAC CCT CTG TTG ACC TGG AGT GAG CAT GCG TTG	Pro Asp Ile Asp Thr Thr His Pro Leu Leu Thr Trp Ser Glu His Ala Leu
GAG ATG TTC TCG GAT GTC AAC GAT GAG GAG CTG ACC CGC ATG TGG TCG	Glu Met Phe Ser Asp Val Val Asn Gln Thr Trp Phe Tyr Phe Arg Met Trp Ser
CGT TTC ATG GTC CTG AAC CAG ACC TGG TTT TAC TTC CCC ATT CTC TCG	Arg Phe Met Val Leu Leu Asn Gln Thr Trp Phe Tyr Phe Pro Ile Leu Ser
TTT GCC CGT CTC TCC TGG TGC CTC CAG TCC ATT CTC TTT GTG CTG CCT	Phe Ala Arg Leu Ser Trp Cys Leu Gln Ser Ile Leu Phe Val Leu Pro
AAC GGT CAG GCC CAC AAG CCC TCG GGC GCG CGT GTG CCC ATC TCG TTG	Asn Gly Gln Ala His Lys Lys Pro Ser Ser Gly Ala Arg Val Pro Ile Ser Leu
GTC GAG CAG CTG TCG CTT GCG ATG CAC TGG ACC TGG TAC CTC GCC ACC	Val Glu Gln Leu Ser Leu Leu Ala Met His Trp Thr Trp Tyr Leu Ala Thr
ATG TTC CTG TTC ATC AAG GAT CCC GTC AAC ATG CTG GTG TAC TTT TTG	Met Phe Leu Phe Ile Lys Asp Pro Val Val Asn Met Leu Val Tyr Phe Leu
GTG TCG CAG GCG GTG TGC GGA AAC TTG TTG GCG ATC GTG TTC TCG CTC	Val Ser Gln Ala Val Cys Gly Gly Asn Leu Leu Ala Ile Val Phe Ser Leu

FIG. 3C

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AAC CAC AAC GGT ATG CCT GTG ATC TCG AAG GAG GCG GTC GAT ATG
 Asn His Asn Gly Met Pro Val Ile Ser Lys Glu Glu Ala Val Asp Met

1140 *
 GAT TTC TTC ACG AAG CAG ATC ATC ACG GGT CGT GAT GTC CAC CCG GGT
 Asp Phe Phe Thr Thr Lys Lys Gln Ile Ile Thr Gly Arg Asp Val His Pro Gly

1200 *
 CTA TTT GCC AAC TGG TTC ACG GGT GGA TTG AAC TAT CAG ATC GAG CAC
 Leu Phe Ala Asn Trp Phe Thr Gly Gly Leu Asn Tyr Gln Ile Glu His

1260 *
 CAC TTG TTC CCT TCG ATG CCT CGC CAC AAC TTT TCA AAG ATC CAG CCT
 His Leu Phe Pro Ser Met Pro Arg His Asn Phe Ser Lys Ile Gln Pro

1320 *
 GCT GTC GAG ACC CTG TGC AAA AAG TAC AAT GTC CGA TAC CAC ACC ACC
 Ala Val Glu Thr Leu Cys Lys Lys Tyr Asn Val Arg Tyr His Thr Thr

1380 *
 GGT ATG ATC GAG GGA ACT GCA GAG GTC TTT AGC CGT CTG AAC GAG GTC
 Gly Met Ile Glu Gly Thr Ala Glu Val Phe Ser Arg Leu Asn Glu Val

1440 *
 TCC AAG GCT GCC TCC AAG ATG GGT AAG GCG CAG TAA A A A A A A A A A C A A G G A C
 Ser Lys Ala Ala Ser Lys Lys Met Gly Lys Ala Gln

FIG. 3D

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1500 *
GTTTTTTTC GCCAGTGCCT GTGCCTGTGC CTGCTTCCCT TGTCAAGTCG AGCGTTTCTG
1560 *
GAAAGGATCG TTCAGTGCAG TATCATCATT CTCCTTTTAC CCCCCGCTCA TATCTCATTC
ATTCTCTTA TTAACAACCT TGTCCCCCC TTCAACCG

FIG. 3E

Ma524	EVRKRLTLFQSLGYDSSKAYYAFKVSFNL	CIWGLSTVI	IVAKWGQTS	TLANVLS	AALLGL	90
ATTS4723	- - - - -	VTLY - TLA	FVAAMSLG	VL	YGVLACPS	VXPHQIAAGLLGL 38
12-5	- - - - -	- - - - -	- - - - -	GVLYGVLAC	TSVFAHQIA	AALLGL 24
T42806	- - - - -	- - - - -	- - - - -	- - - - -	- - - - -	- - - - - 4
W28140	- - - - -	- - - - -	- - - - -	- - - - -	- - - - -	- - - - - 1
R05219	- - - - -	- - - - -	- - - - -	- - - - -	- - - - -	- - - - - 2
W53753	- - - - -	- - - - -	- - - - -	- - - - -	- - - - -	- - - - - 1

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Ma524	FWQQCGWLAHDFLHHQVFQDRFWGDL	FGAFLGGVC	-	QGFSSSWWKDKHNT	HHAAPNVHGE	119
ATTS4723	LWIIQSA	YIGXDSG	HYVIMSNKSNNX	-	FAQLLSGNCLTG	I IAWWKWTHNAHHLACNSLDY 97
12-5	LWIIQSA	YIGXDSG	HYVIMSNKSYNR	-	FAQLLSGNCLTG	IS IAWWKWTHNAHHLACNSLDY 83
T42806	- - - - -	- - - - -	- - - - -	- - - - -	- - - - -	- - - - - 4
W28140	- - - - -	- - - - -	- - - - -	- - - - -	- - - - -	- - - - - 1
R05219	- - - - -	- - - - -	- - - - -	- - - - -	- - - - -	- - - - - 2
W53753	- - - - -	- - - - -	- - - - -	- - - - -	- - - - -	- - - - - 1

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Ma524	DPDIDTHPLLTWSEHALEMFS	SDVPDEELTRMWS	- - - - -	RFMV	LNQTWFFYPILSFARLSW	174
ATTS4723	GP	NLQH	IIP	- - - - -	- - - - -	105
12-5	DPD	LQH	IIP	VFAV	STK - - - - -	FSS
T42806	- - - - -	- - - - -	- - - - -	- - - - -	- - - - -	- - - - - 4
W28140	- - - - -	- - - - -	- - - - -	- - - - -	- - - - -	- - - - - 1
R05219	- - - - -	- - - - -	- - - - -	- - - - -	- - - - -	- - - - - 2
W53753	- - - - -	- - - - -	- - - - -	- - - - -	- - - - -	- - - - - 1

FIG. 4A

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Ma524	CLQSI L F V L P N G Q A H K P S G A R V P I S L V E Q L S L A M	129
ATTS4723	W W H W T W Y L A T M F L F I K D P V N M L V	105
12-5	F I Q T F L L F S K R E	185
T42806	V P D R A L N F A G I L V	29
W28140	N F A G I L V	33
R05219	P A T E V G G L A W M I T - Y - R F F L T Y V P L L G L K A F	2
W53753	F - S	48
	R H E A R G G T R L A Y M L V C M Q W T D L - L W A A S Y R F F L S Y S P F Y G A T G T	
Ma524	Y F L V S Q A V C G N L L A I V F S L N H N G M P V I S K E E A V D M D F F T K Q I I T G R D V H P G L F A N W F T G G	289
ATTS4723		105
12-5	F F V F T S F T V T A L Q H I Q F T L N H F A A D V Y V - G P P T G S D W F E K Q A A G T I D I S C R S Y M D W F F G G	244
T42806	X F V F T G F T V T A L Q H I Q F T L N H F A A D V Y V - G P P T G S D W F E K Q A A G T I D I S C R S Y M D W F F G G	88
W28140	L F I V R F L E S N W F V W V T Q M N H - - I P M H I D H D R N M D W V S T Q L Q A T C N V H K S A F N I D W F S G H	90
R05219		23
W53753	L F V A V R V L E S H W F V W I T Q M N H - - I P K E I G H E K H R D W A S S Q L A A T C N V E P S L F D W F S G H	105
Ma524	L N Y Q I E H H L F P S M P R H N F S K I Q P A V E T L C K K Y N V R Y H T T G M I E G T A E V E S R L N E V S K A A S	349
ATTS4723		105
12-5	L Q F Q L E H H	252
T42806	L Q F Q L E H H L F P R L P R C H L R K V S P V G Q R G F Q R K X N L S X	125
W28140	L N F Q I E H H L F P T M P R H N Y H X V A P L V Q S L C A K H G I E Y Q S K P L	131
R05219	L N Y Q I E H H L F P T M P R C N L N R C M K Y V K E W C A E N I L P Y L V D D Y F V G Y N L N L Q Q L K N M A E L V Q	83
W53753	L N F Q I E H H L F P T M P R H N Y R X V A P L V K A F C A K H G L H Y E V	143
Ma524	K M G K A Q	355
ATTS4723		105
12-5	- - A K A	252
T42806		125
W28140		131
R05219		87
W53753		148

FIG. 4B

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```

60 *
GTCCCCTGTC GCTGTCGGCA CACCCCATCC TCCCTCGCTC CCTCTGCGTT TGTCCTTGGC
120 *
CCACCGTCTC TCCTCCACCC TCCGAGACGA CTGCAACTGT AATCAGGAAC CGACAAATAC
180 *
ACGATTTCTT TTTACTCAGC ACCAACTCAA AATCCTCAAC CGCAACCCTT TTTCAGG ATG
Met
GCA CCT CCC AAC ACT ATC GAT GCC GGT TTG ACC CAG CGT CAT ATC AGC
Ala Pro Pro Asn Thr Ile Asp Ala Gly Leu Thr Arg Gln Arg His Ile Ser
240 *
ACC TCG GCC CCA AAC TCG GCC AAG CCT GCC TTC GAG CGC AAC TAC CAG
Thr Ser Ala Pro Asn Ser Ala Lys Pro Ala Phe Glu Arg Asn Tyr Gln
300 *
CTC CCC GAG TTC ACC ATC AAG GAG ATC CGA GAG TGC ATC CCT GCC CAC
Leu Pro Glu Phe Thr Ile Lys Glu Ile Arg Glu Cys Ile Pro Ala His
360 *
TGC TTT GAG CGC TCC GGT CTC CGT GGT CTC TGC CAC GGT GCC ATC GAT
Cys Phe Glu Arg Ser Gly Leu Arg Gly Leu Cys His Val Ala Ile Asp
420 *
CTG ACT TGG GCG TCG CTC TTG TTC CTG GCT GCG ACC CAG ATC GAC AAG
Leu Thr Trp Ala Ser Leu Leu Phe Leu Ala Ala Thr Gln Ile Asp Lys
TTT GAG AAT CCC TTG ATC CGC TAT TTG GCC TGG CCT GTT TAC TGG ATC
Phe Glu Asn Pro Leu Ile Arg Tyr Leu Ala Trp Pro Val Tyr Trp Ile

```

FIG. 5A

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ATG Met	CAG Gln	GGT Gly	ATT Ile	GTC Val	TGC Cys	ACC Thr	GGT Gly	GTC Val	TGG Trp	GTG Val	CTG Leu	GCT Ala	CAC His	GAG Glu	TGT Cys
			480*				540*								
GGT Gly	CAT His	CAG Gln	TCC Ser	TTC Phe	TCG Ser	ACC Thr	TCC Ser	AAG Lys	ACC Thr	CTC Leu	AAC Asn	AAC Asn	ACA Thr	GTT Val	GGT Gly
											600*				
TGG Trp	ATC Ile	TTG Leu	CAC His	TCG Ser	ATG Met	CTC Leu	TTG Leu	GTC Val	CCC Pro	TAC Tyr	CAC His	TCC Ser	TGG Trp	AGA Arg	ATC Ile
															660*
TCG Ser	CAC His	TCG Ser	AAG Lys	CAC His	CAC His	AAG Lys	GCC Ala	ACT Thr	GGC Gly	CAT His	ATG Met	ACC Thr	AAG Lys	GAC Asp	CAG Gln
GTC Val	TTT Phe	GTG Val	CCC Pro	AAG Lys	ACC Thr	CGC Arg	TCC Ser	CAG Gln	GTT Val	GGC Gly	TTG Leu	CCT Pro	CCC Pro	AAG Lys	GAG Glu
AAC Asn	GCT Ala	GCT Ala	GCT Ala	GCT Ala	GTT Val	CAG Gln	GAG Glu	GAG Glu	GAC Asp	ATG Met	TCC Ser	GTG Val	CAC His	CTG Leu	GAT Asp
GAG Glu	GAG Glu	GCT Ala	CCC Pro	ATT Ile	GTG Val	ACT Thr	TTG Leu	TTC Phe	TGG Trp	ATG Met	GTG Val	ATC Ile	CAG Gln	TTC Phe	TTG Leu
TTC Phe	GGA Gly	TGG Trp	CCC Pro	GCG Ala	TAC Tyr	CTG Leu	ATT Ile	ATG Met	AAC Asn	GCC Ala	TCT Ser	GGC Gly	CAA Gln	GAC Asp	TAC Tyr

FIG. 5B

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GGC Gly	CGC Arg	TGG Trp	ACC Thr	TCG Ser	CAC His	TTC Phe	CAC His	ACG Thr	TAC Tyr	TCG Ser	CCC Pro	ATC Ile	TTT Phe	GAG Glu	CCC Pro	900 *
CGC Arg	AAC Asn	TTT Phe	TTT Phe	GAC Asp	ATT Ile	ATT Ile	ATC Ile	TCG Ser	GAC Asp	CTC Leu	GGT Gly	GTG Val	TTG Leu	GCT Ala	GCC Ala	
CTC Leu	GGT Gly	GCC Ala	CTG Leu	ATC Ile	TAT Tyr	GCC Ala	TCC Ser	ATG Met	CAG Gln	TTG Leu	TCG Ser	CTC Leu	TTG Leu	ACC Thr	GTC Val	
ACC Thr	AAG Lys	TAC Tyr	TAT Tyr	ATT Ile	GTC Val	CCC Pro	TAC Tyr	CTC Leu	TTT Phe	GTC Val	AAC Asn	TTT Phe	TGG Trp	TTG Lru	GTC Val	
CTG Leu	ATC Ile	ACC Thr	Phe Thr	TTG Leu	Gln Gln	CAC His	ACC Thr	GAT Asp	CCC Pro	AAG Lys	CTG Leu	CCC Pro	CAT His	TAC Tyr	CGC Arg	1080 *
GAG Glu	GGT Gly	GCC Ala	TGG Trp	AAT Asn	TTC Phe	CAG Gln	CGT Arg	GGA Gly	GCT Ala	CTT Leu	TGC Cys	ACC Thr	GTT Val	GAC Asp	CGC Arg	1140 *
TCG Ser	TTT Phe	GGC Gly	AAG Lys	TTC Phe	TTG Leu	GAC Asp	CAT His	ATG Met	TTC Phe	CAC His	GGC Gly	ATT Ile	GTC Val	CAC His	ACC Thr	
CAT His	GTG Val	GCC Ala	CAT His	CAC His	TTG Leu	TTC Phe	TTC Ser	CAA Met	ATG Met	CCG Pro	TTC Phe	TAC Tyr	CAT His	GCT Ala	GAG Glu	

FIG. 5C

09/367013

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```

1260 *
GAA GCT ACC TAT CAT CTC AAG AAA CTG CTG GGA GAG TAC TAT GTG TAC
Glu Ala Thr Tyr His Leu Lys Lys Leu Leu Gly Glu Tyr Val Tyr

1320 *
GAC CCA TCC CCG ATC GTG GTT GCG GTC TGG AGG TCG TTC CGT GAG TGC
Asp Pro Ser Pro Ile Val Val Ala Val Trp Arg Ser Phe Arg Glu Cys

1380 *
CGA TTC GTG GAG GAT CAG GGA GAC GTG GTC TTT TTC AAG AAG TAAAAA
Arg Phe Val Glu Asp Gln Gly Asp Val Val Phe Phe Lys Lys

1440 *
AAAAGACAAT GGACCACACA CAACCTTGTC TCTACAGACC TACGTATCAT GTAGCCATAC

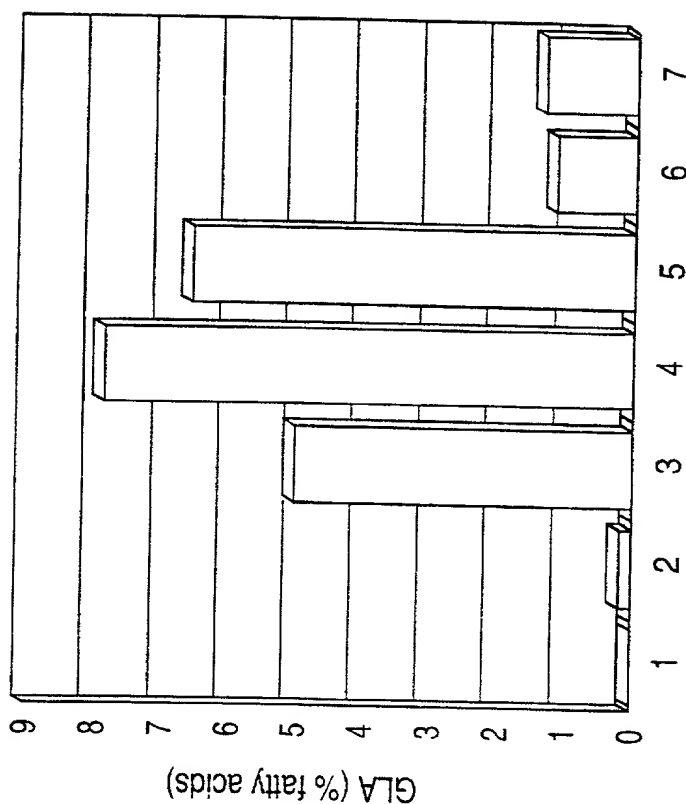
CACTTCATAA AGAACATGA GCTCTAGAGG CGTGTCATTC GCGCCTCC

```

FIG. 5D

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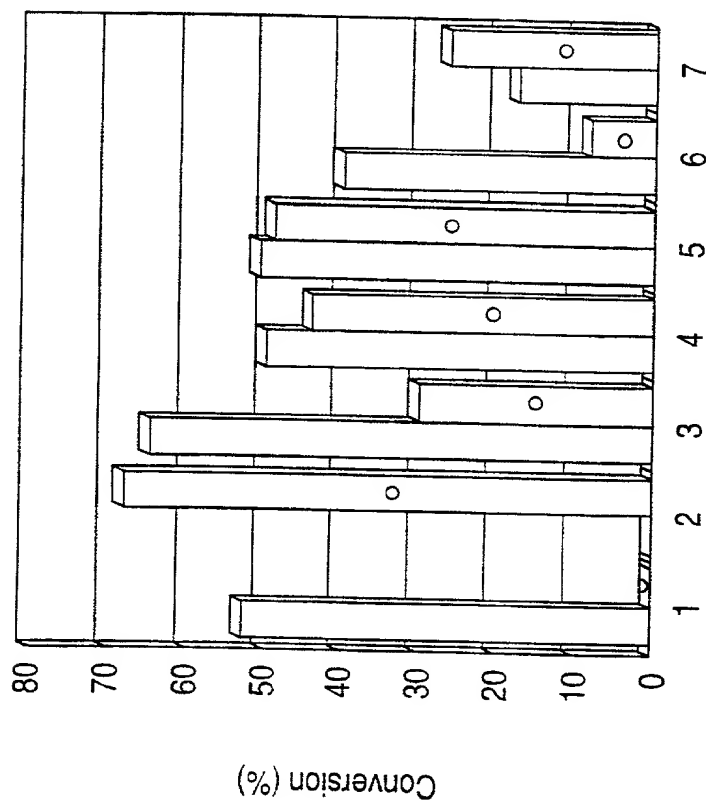
□ GLA



Constructs

FIG. 6B

□ 18:1 to 18:2
○ 18:2 to 18:3



Constructs

FIG. 6A

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□ GLA

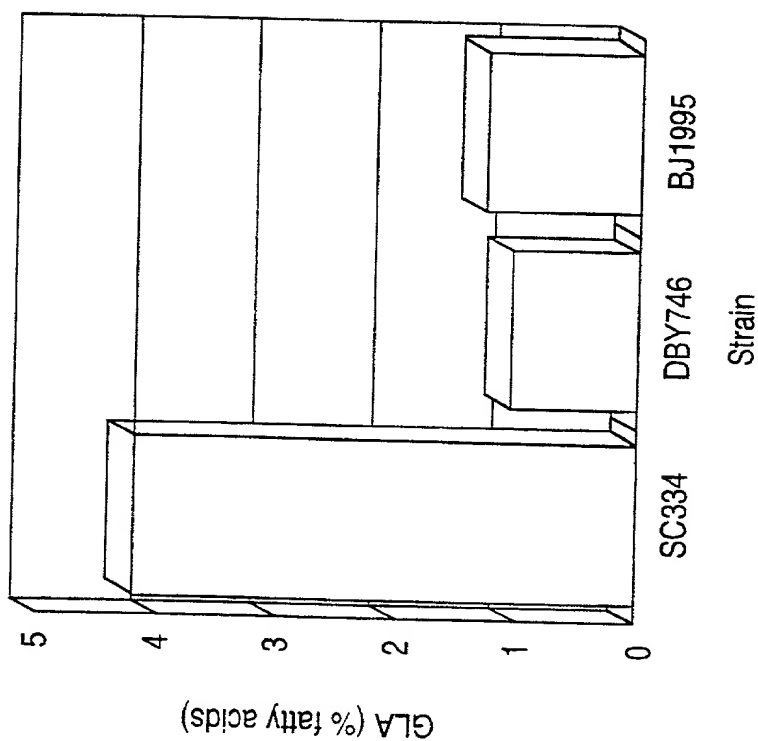


FIG. 7B

□ 18:1 to 18:2
○ 18:2 to 18:3

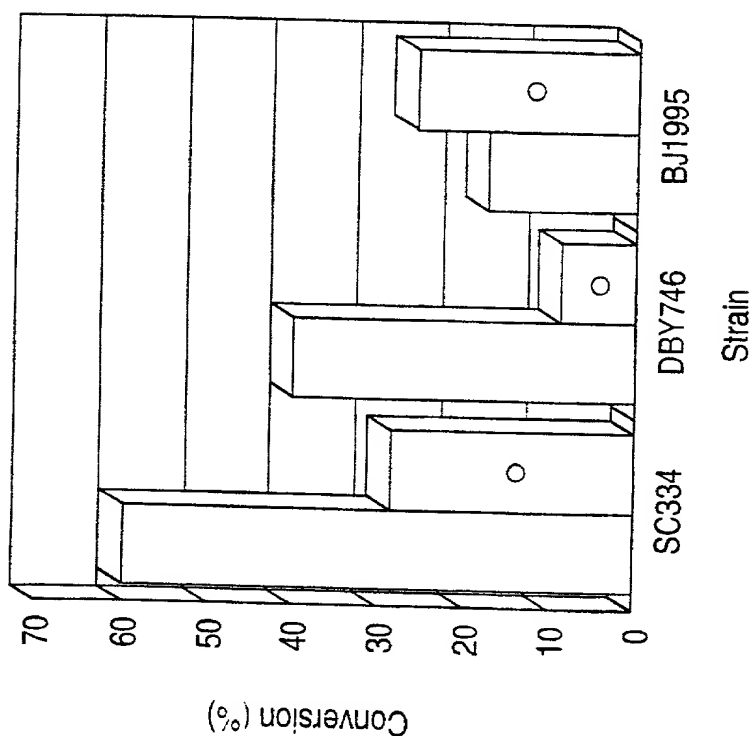


FIG. 7A

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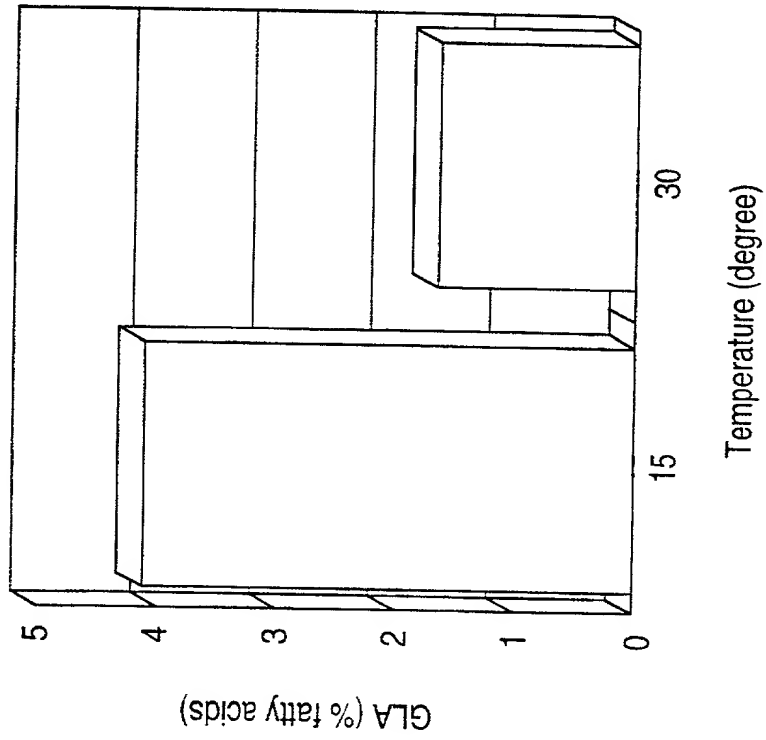


FIG. 8B

□ 18:1 to 18:2
○ 18:2 to 18:3

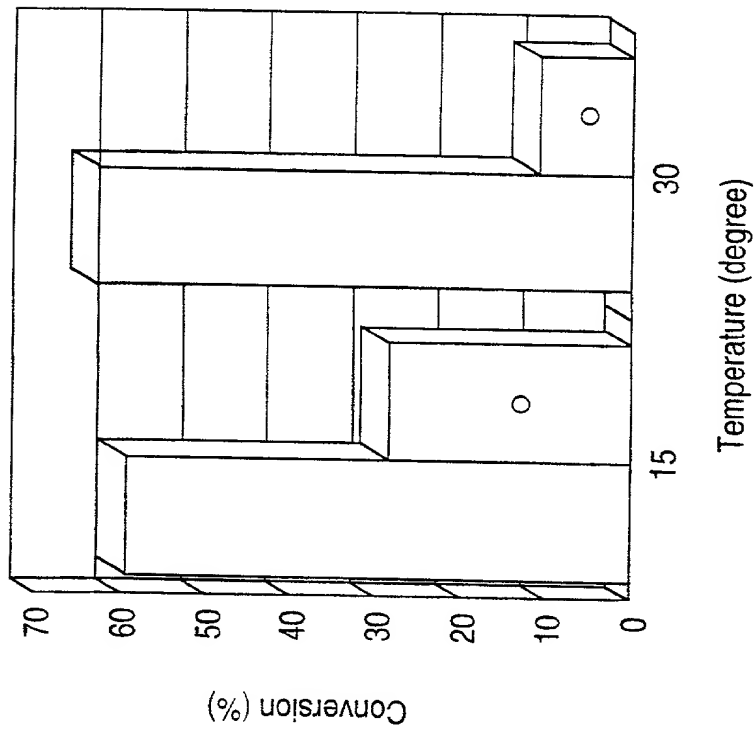


FIG. 8A

SCORES INIT1: 117 INITN: 225 OPT: 256
SMITH-WATERMAN SCORE: 408; 27.0% IDENTITY IN 441 aa OVERLAP

[illegible]

ma29gcg.pep
PVFEMYHAF - GAADA IMKKYYVGT LVSNELP I FPEPTVFHKTIKTRVEGYFTDRN IDPKN
DPF VAFHINKGL VKKYMNSLLIGEL - SPEQPSF - EPTKNKELTDFREL RATVERMGLMK

60 70 80 90 100 110
60 70 80 90 100 110

ma29gcg.pep
RPEIWGRYALIFGSLIASYYAQLFVPFVVERTWLQVVF-AIIMGFACAQVGLNPLHDASH
253538a
ANHVF--FLLYLLHILLDGAAWLTLWVFGTSFLPFLCAVLLSAVQAQAGWLQ-HDYGH

```

ma29gcg.pep      180          190          200          210          220
FSVTHNPTVWKILGATHDF- - - FNGASYLVWMYQHMLGHHPTYNIAGADPDVSTSE- - -
:| | :| | |:| | | :| | | :| | | :| | | :| | | :| | | :| | | :| | |
253538a         180          190          200          210          220
LSVYRKPK-WNHL--VHKFVIGHLKGASANWNNHRR-FQHHAKPNI FHKDPDVNMMLHVVFV

```

FIG. 9A

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SCORES INIT1: 117 INITN: 225 OPT: 256
SMITH-WATERMAN SCORE: 408; 27.0% IDENTITY IN 441 aa OVERLAP

ma29gcg.pep	230	240	250	260	270	280
	---PDVRR	IKPNQKWF	-VNHI	NQHMFV	--PFLYGLL	AFKVRIQDINILYFVKTNDAIRV
	:	:	:	:	:	:
253538a	LGEWQPI	EYGKKK	KLKYL	PNYHQHE	YFFLIGP	PLIPMYFQYQI-----IMTMI
	230	240	250	260	270	280
ma29gcg.pep	290	300	310	320	330	340
	NPIS	TWHTVM	FWGKAFF	VWYRLI	VPLQYPL	GKVL
	:	:	:	:	:	:
253538a	---AWA	VSYYI	---RFF	ITY---	IPF-YG	ILG-ALLFLNFI
	290	300	310	320	330	340
ma29gcg.pep	350	360	370	380	390	
	EEVQW	PLPDENG	I	QKDWAA	MQVETT	-----QDYA
	:	:	:	:	:	:
253538a	MEI	-----DQ	EAY--	RDWFSS	QLTATCN	VEQSFFND---WFS---GHLNFQIEHHLFPTMP
	340	350	360	370	380	390
ma29gcg.pep	400	410	420	430	440	
	QHHYP	DI	LAII	KNTCSE	YKVPYL	VKDTFWQAF
	:	:	:	:	:	:
253538a	RHNLH	KI	APLVK	SLCAKH	GI	EYQEKPLLRALDI
	380	390	400	410	420	430
						IRSLKKS
						GLWLDAYLHKX

FIG. 9B

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SCORES INIT1: 231 INITN: 499 OPT: 401
SMITH-WATERMAN SCORE: 620; 27.3% IDENTITY IN 455 aa OVERLAP

ma524gcg.pep	10	20	30	40	50	59
	MAAAPSVRTFTRAEVLNAEALNEGKKDAEAPFLMIDNKVYDVREFVPDHPGGSVILTH-					
	: : : :	: :	: : :	: : :	: : :	: : :
253538a	10	20	30	40	50	
	QGPTPRYFTWDEV-----AQRSGCEERWLVIDRKVYNI SEFTRRHPPGGSRVISHY					
	: : : :	: :	: : :	: : :	: : :	: : :
ma524gcg.pep	60	70	80	90	100	110
	VGKDGTDVFDTFHPEAAW--ETLANFYVGDI DE---SDRDIKNDDFAAEVRKLRITLFSQL					
	: : : :	: :	: : :	: : :	: : :	: : :
253538a	60	70	80	90	100	110
	AGQDATDPFVAFHINKGLVKKYMNSLLIGELSPEQPSFEPTKNKELTDEFRELRAVERM					
	: : : :	: :	: : :	: : :	: : :	: : :
ma524gcg.pep	120	130	140	150	160	170
	GYDSSSKAYYAFKVSFNLCIWGLSTVIVAKWGQSTLANVLSAALLGLFWQQCGWLAHDF					
	: : : :	: :	: : :	: : :	: : :	: : :
253538a	120	130	140	150	160	
	GLMKANHVVFFLLYLHILLDGAAWLTLWVFG-TSFLPFLLCVLLSAVQAQAGWLQHDY					
	: : : :	: :	: : :	: : :	: : :	: : :
ma524gcg.pep	180	190	200	210	220	230
	LHHQVFQDRFWGDLFGAFLGGVCQGFSSSWWKDKHNTTHHAAPNVHGEDPDIDTHPLL TWS					
	: : : :	: :	: : :	: : :	: : :	: : :
253538a	170	180	190	200	210	220
	GHLSVYRKPKWNHLVHKFVIGHLKGASANWNHRHFQHHAKPNI FHKDPDVN---ML----					
	: : : :	: :	: : :	: : :	: : :	: : :

SUBSTITUTE SHEET (RULE 26)

FIG. 10A

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SCORES INIT1: 231 INITN: 499 OPT: 401
SMITH-WATERMAN SCORE: 620; 27.3% IDENTITY IN 455 aa OVERLAP

ma524gcg.pep	240	250	260	270	280	290
	EHALEMFSDVPDEELTRMWSR	FMLNQTWFYF	ILS---	FARLSWCLQS	ILFVLPNGQAH	
253538a	-HVF-VLGEWQPI	EYGKKKLLKYL	PYNHQHEFFL	IGPPLLIPMYFQYQ	IIMTMI----	VH
	230	240	250	260	270	
ma524gcg.pep	300	310	320	330	340	349
	KPSGARVPISLVEQLSLAMHWTWYLA	TMFLFIK--	DPVNMLVYFLVSQAVCGNLLA	IVFS		
253538a	K-----	NWVDLAWAVSYYIRFFITYIPFYGILGALLFLNFIRFLESHWVFWVTQ				
	280	290	300	310	320	
ma524gcg.pep	350	360	370	380	390	400
	LNHNMGMPVISKEEAVDMDFFFTKQIITGRDVHPGLFANWFTGGLNYQIEHHLFPSMPRHNF					
253538a	MNHI VMEI--	DQEAYR-DWFFSSQLTATCNVEQSFNDWFSGHLNFQIEHHLFPTMPRHNL				
	330	340	350	360	370	380
ma524gcg.pep	410	420	430	440	450	
	SKIQPAVETLCKKYNVRYHTTGMIEGTAEVFSRLNEVSKAASKMGKAQX					
253538a	HKIAPLVKSLCAKHGIEYQEKPLLRALLD	IRSLKKGKWLWDAYLHKX				
	390	400	410	420	430	

FIG. 10B

Atty Docket No. CGAB-210 USA**COMBINED DECLARATION FOR PATENT APPLICATION AND POWER OF ATTORNEY**

As a below named inventor, I hereby declare that:

My residence, post office address and citizenship are as stated below next to my name,

I believe I am the original, first and sole inventor (if only one name is listed below) or an original, first and joint inventor (if plural names are listed below) of the subject matter which is claimed and for which a patent is sought on the invention entitled

METHODS AND COMPOSITIONS FOR SYNTHESIS OF LONG CHAIN POLYUNSATURATED FATTY ACIDS

the specification of which (check one) ☐ is attached hereto or ☒ was filed on 10 April 1998 as International Application No. PCT/US98/07126 and was amended on _____ (if applicable).

I hereby state that I have reviewed and understand the contents of the above-identified specification, including the claims, as amended by any amendment referred to above.

I acknowledge the duty to disclose all information which is material to patentability as defined in 37 CFR § 1.56.

I hereby claim foreign priority benefits under 35 U.S.C. § 119(a)-(d) or § 365(b) of any foreign application(s) for patent or inventor's certificate, or § 365(a) of any PCT International application which designated at least one country other than the United States, listed below and have also identified below any foreign application for patent or inventor's certificate having a filing date before that of the application on which priority is claimed:

Prior Foreign Application(s)			Priority Claimed	
			Yes	No
Number	Country	Day/Month/Year Filed		
Number	Country	Day/Month/Year Filed		

I hereby claim the benefit under 35 U.S.C. § 119(e) of any United States provisional application(s) below.

Application Number	Filing Date

I hereby claim the benefit under 35 U.S.C. § 120 of any United States application(s), or § 365(c) of any PCT International application designating the United States, listed below and, insofar as the subject matter of each of the claims of this application is not disclosed in the prior United States application in the manner provided by the first paragraph of 35 U.S.C. § 112, I acknowledge the duty to disclose all information which is material to patentability as defined in 37 CFR § 1.56 which became available between the filing date of the prior application and the national or PCT international filing date of this application:

<u>08/834,655</u>	<u>11 April 1997</u>	<u>Pending</u>
Application Number	Filing Date	Status: Patented, Pending, Abandoned
Application Number	Filing Date	Status: Patented, Pending, Abandoned

I HEREBY APPOINT THE FOLLOWING AS MY ATTORNEYS WITH FULL POWER OF SUBSTITUTION TO PROSECUTE THIS APPLICATION AND TRANSACT ALL BUSINESS IN THE PATENT OFFICE CONNECTED THEREWITH:

Karl A. Limbach	18,689	W. Patrick Bengtsson	32,456	Kyla L. Harriel	P-41,816
George C. Limbach	19,305	Mark A. Dalla Valle	34,147	Mayumi Maeda	40,075
John K. Uilkema	20,282	Charles P. Sammut	28,901	Kent J. Tobin	39,496
Neil A. Smith	25,441	Mark C. Pickering	36,239	Christine S. Ring	P-42,106
Veronica C. Devitt	29,375	Kathleen A. Frost	37,326	Michael R. Ward	38,651
Ronald L. Yin	27,607	Alan S. Hodes	38,185	Steven M. Santisi	40,157
Gerald T. Sekimura	30,103	Patricia Coleman James	37,155	Charles L. Hamilton	P-42,624
Michael A. Stallman	29,444	Alan A. Limbach	39,749	Andrew V. Smith	P-43,132
Philip A. Girard	28,848	Douglas C. Limbach	35,249	Heath W. Hoglund	41,076
Michael J. Pollock	29,098	Brian J. Keating	39,520	J. Thomas McCarthy	22,420
Stephen M. Everett	30,050	Seong-Kun Oh*			
Alfred A. Equitz	30,922	Cameron A. King	P-41,897		

* Recognition under 37 CFR 10.9(b)

Send correspondence to Limbach & Limbach L.L.P.
Attn: Michael R. Ward
2001 Ferry Building
San Francisco, CA 94111
Telephone: 415/433-4150

I hereby declare that all statements made herein of my own knowledge are true and that all statements made on information and belief are believed to be true; and further that these statements were made with the knowledge that willful false statements and the like so made are punishable by fine or imprisonment or both, under 18 U.S.C. § 1001 and that such willful false statements may jeopardize the validity of the application or any patent issued thereon.

Full name of sole or first inventor DEBORAH KNUTZON

Inventor's signature _____

Date _____

Residence 6110 Rockhurst Way, Granite Bay, California 95746

Citizenship U.S.A.

Post Office Address 6110 Rockhurst Way, Granite Bay, California 95746

2-00
Full name of second joint inventor, if any, PRADIP MUKERJI

Inventor's signature _____

8/4/98
Date OH

Residence 1069 Arcaro Drive, Gahanna, Ohio 43230

Citizenship ~~Republic of China, Canada~~ U.S.A

Post Office Address 1069 Arcaro Drive, Gahanna, Ohio 43230

I HEREBY APPOINT THE FOLLOWING AS MY ATTORNEYS WITH FULL POWER OF SUBSTITUTION TO PROSECUTE THIS APPLICATION AND TRANSACT ALL BUSINESS IN THE PATENT OFFICE CONNECTED THEREWITH:

33

Karl A. Limbach	<u>18,689</u>	W. Patrick Bengtsson	<u>32,456</u>	Kyla L. Harriel	<u>P-41,816</u>
George C. Limbach	<u>19,305</u>	Mark A. Dalla Valle	<u>34,147</u>	Mayumi Maeda	<u>40,075</u>
John K. Uilkema	<u>20,282</u>	Charles P. Sammut	<u>28,901</u>	Kent J. Tobin	<u>39,496</u>
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Veronica C. Devitt	<u>29,375</u>	Kathleen A. Frost	<u>37,326</u>	Michael R. Ward	<u>38,651</u>
Ronald L. Yin	<u>27,607</u>	Alan S. Hodes	<u>38,185</u>	Steven M. Santisi	<u>40,157</u>
Gerald T. Sekimura	<u>30,103</u>	Patricia Coleman James	<u>37,155</u>	Charles L. Hamilton	<u>P-42,624</u>
Michael A. Stallman	<u>29,444</u>	Alan A. Limbach	<u>39,749</u>	Andrew V. Smith	<u>P-43,132</u>
Philip A. Girard	<u>28,848</u>	Douglas C. Limbach	<u>35,249</u>	Heath W. Hoglund	<u>41,076</u>
Michael J. Pollock	<u>29,098</u>	Brian J. Keating	<u>39,520</u>	J. Thomas McCarthy	<u>22,420</u>
Stephen M. Everett	<u>30,050</u>	Seong-Kun Oh*			
Alfred A. Equitz	<u>30,922</u>	Cameron A. King	<u>P-41,897</u>		

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2001 Ferry Building
San Francisco, CA 94111
Telephone: 415/433-4150

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1-00
Full name of sole or first inventor DEBORAH KNUTZON

Inventor's signature Deborah Knutzon

8/4/98
Date

Residence 6110 Rockhurst Way, Granite Bay, California 95746

Citizenship U.S.A.

Post Office Address 6110 Rockhurst Way, Granite Bay, California 95746

2-00
Full name of second joint inventor, if any, PRADIP MUKERJI

Inventor's signature _____

Date

Residence 1069 Arcaro Drive, Gahanna, Ohio 43230

Citizenship Republic of China, Canada

Post Office Address 1069 Arcaro Drive, Gahanna, Ohio 43230

Atty Docket No. CGAB-210 USA**COMBINED DECLARATION FOR PATENT APPLICATION AND POWER OF ATTORNEY**

As a below named inventor, I hereby declare that:

My residence, post office address and citizenship are as stated below next to my name,

I believe I am the original, first and sole inventor (if only one name is listed below) or an original, first and joint inventor (if plural names are listed below) of the subject matter which is claimed and for which a patent is sought on the invention entitled

METHODS AND COMPOSITIONS FOR SYNTHESIS OF LONG CHAIN POLYUNSATURATED FATTY ACIDS

the specification of which (check one) ☐ is attached hereto or ☒ was filed on 10 April 1998 as International Application No. PCT/US98/07126 and was amended on _____ (if applicable).

I hereby state that I have reviewed and understand the contents of the above-identified specification, including the claims, as amended by any amendment referred to above.

I acknowledge the duty to disclose all information which is material to patentability as defined in 37 CFR § 1.56.

I hereby claim foreign priority benefits under 35 U.S.C. § 119(a)-(d) or § 365(b) of any foreign application(s) for patent or inventor's certificate, or § 365(a) of any PCT International application which designated at least one country other than the United States, listed below and have also identified below any foreign application for patent or inventor's certificate having a filing date before that of the application on which priority is claimed:

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			Yes	No
Number	Country	Day/Month/Year Filed	_____	_____
Number	Country	Day/Month/Year Filed	_____	_____

I hereby claim the benefit under 35 U.S.C. § 119(e) of any United States provisional application(s) below.

Application Number	Filing Date
_____	_____

Application Number	Filing Date
_____	_____

I hereby claim the benefit under 35 U.S.C. § 120 of any United States application(s), or § 365(c) of any PCT International application designating the United States, listed below and, insofar as the subject matter of each of the claims of this application is not disclosed in the prior United States application in the manner provided by the first paragraph of 35 U.S.C. § 112, I acknowledge the duty to disclose all information which is material to patentability as defined in 37 CFR § 1.56 which became available between the filing date of the prior application and the national or PCT international filing date of this application:

08/834,655	11 April 1997	Pending
Application Number	Filing Date	Status: Patented, Pending, Abandoned
_____	_____	_____
Application Number	Filing Date	Status: Patented, Pending, Abandoned

3-00

Full name of third joint inventor, if any, YUNG-SHENG HUANG

Inventor's signature _____

Date

Residence 2462 Danvers Court, Upper Arlington, Ohio 43220

OH

Citizenship U.S.A.

Post Office Address 2462 Danvers Court, Upper Arlington, Ohio 43220

4-00

Full name of fourth joint inventor, if any, JENNIFER THURMOND

Inventor's signature _____

Date

Residence 3702 Adirondack, Columbus, Ohio 43231

OH

Citizenship U.S.A.

Post Office Address 3702 Adirondack, Columbus, Ohio 43231

5-00

Full name of fifth joint inventor, if any, SUNITA CHAUDHARY

Inventor's signature _____

Date

Residence 3419 Woodbine Place, Pearland, Texas 77584

TX

Citizenship India

Post Office Address 3419 Woodbine Place, Pearland, Texas 77584

6-00

Full name of sixth joint inventor, if any, AMANDA EUN-YEONG LEONARD

Inventor's signature _____

Date

Residence 581 Shadewood Court, Gahanna, Ohio 43230

Citizenship U.S.A.

Post Office Address 581 Shadewood Court, Gahanna, Ohio 43230

3-00
Full name of third joint inventor, if any, YUNG-SHENG HUANG
Inventor's signature Y-S. Huang Date 8/4/98
Residence 2462 Danvers Court, Upper Arlington, Ohio 43220
Citizenship U.S.A. Taiwan, Canada
Post Office Address 2462 Danvers Court, Upper Arlington, Ohio 43220

4-00
Full name of fourth joint inventor, if any, JENNIFER THURMOND
Inventor's signature Jennifer Thurmond Date 8-4-98
Residence 3072 Adirondack, Columbus, Ohio 43231
Citizenship U.S.A.
Post Office Address 3072 Adirondack, Columbus, Ohio 43231
3072

Full name of fifth joint inventor, if any, SUNITA CHAUDHARY
Inventor's signature _____ Date _____
Residence 3419 Woodbine Place, Pearland, Texas 77584
Citizenship India
Post Office Address 3419 Woodbine Place, Pearland, Texas 77584

6-00
Full name of sixth joint inventor, if any, AMANDA EUN-YEONG LEONARD
Inventor's signature Amanda Eun-yeong Leonard Date 8/4/98
Residence 581 Shadewood Court, Gahanna, Ohio 43230
Citizenship U.S.A.
Post Office Address 581 Shadewood Court, Gahanna, Ohio 43230

Atty Docket No. CGAB-210 USA**COMBINED DECLARATION FOR PATENT APPLICATION AND POWER OF ATTORNEY**

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METHODS AND COMPOSITIONS FOR SYNTHESIS OF LONG CHAIN POLYUNSATURATED FATTY ACIDS

the specification of which (check one) ☐ is attached hereto or ☒ was filed on 10 April 1998 as International Application No. PCT/US98/07126 and was amended on _____ (if applicable).

I hereby state that I have reviewed and understand the contents of the above-identified specification, including the claims, as amended by any amendment referred to above.

I acknowledge the duty to disclose all information which is material to patentability as defined in 37 CFR § 1.56.

I hereby claim foreign priority benefits under 35 U.S.C. § 119(a)-(d) or § 365(b) of any foreign application(s) for patent or inventor's certificate, or § 365(a) of any PCT International application which designated at least one country other than the United States, listed below and have also identified below any foreign application for patent or inventor's certificate having a filing date before that of the application on which priority is claimed:

Prior Foreign Application(s)			Priority Claimed	
			Yes	No
Number	Country	Day/Month/Year Filed	_____	_____
Number	Country	Day/Month/Year Filed	_____	_____

I hereby claim the benefit under 35 U.S.C. § 119(e) of any United States provisional application(s) below.

Application Number	Filing Date
_____	_____

Application Number	Filing Date
_____	_____

I hereby claim the benefit under 35 U.S.C. § 120 of any United States application(s), or § 365(c) of any PCT International application designating the United States, listed below and, insofar as the subject matter of each of the claims of this application is not disclosed in the prior United States application in the manner provided by the first paragraph of 35 U.S.C. § 112, I acknowledge the duty to disclose all information which is material to patentability as defined in 37 CFR § 1.56 which became available between the filing date of the prior application and the national or PCT international filing date of this application:

Application Number	Filing Date	Status: Patented, Pending, Abandoned
<u>08/834,655</u>	<u>11 April 1997</u>	<u>Pending</u>

Application Number	Filing Date	Status: Patented, Pending, Abandoned
_____	_____	_____

I HEREBY APPOINT THE FOLLOWING AS MY ATTORNEYS WITH FULL POWER OF SUBSTITUTION TO PROSECUTE THIS APPLICATION AND TRANSACT ALL BUSINESS IN THE PATENT OFFICE CONNECTED THEREWITH:

Karl A. Limbach	18,689	W. Patrick Bengtsson	32,456	Kyla L. Harriel	P-41,816
George C. Limbach	19,305	Mark A. Dalla Valle	34,147	Mayumi Maeda	40,075
John K. Uilkema	20,282	Charles P. Sammut	28,901	Kent J. Tobin	39,496
Neil A. Smith	25,441	Mark C. Pickering	36,239	Christine S. Ring	P-42,106
Veronica C. Devitt	29,375	Kathleen A. Frost	37,326	Michael R. Ward	38,651
Ronald L. Yin	27,607	Alan S. Hodes	38,185	Steven M. Santisi	40,157
Gerald T. Sekimura	30,103	Patricia Coleman James	37,155	Charles L. Hamilton	P-42,624
Michael A. Stallman	29,444	Alan A. Limbach	39,749	Andrew V. Smith	P-43,132
Philip A. Girard	28,848	Douglas C. Limbach	35,249	Heath W. Hoglund	41,076
Michael J. Pollock	29,098	Brian J. Keating	39,520	J. Thomas McCarthy	22,420
Stephen M. Everett	30,050	Seong-Kun Oh*			
Alfred A. Equitz	30,922	Cameron A. King	P-41,897		

* Recognition under 37 CFR 10.9(b)

Send correspondence to Limbach & Limbach L.L.P.
Attn: Michael R. Ward
2001 Ferry Building
San Francisco, CA 94111
Telephone: 415/433-4150

I hereby declare that all statements made herein of my own knowledge are true and that all statements made on information and belief are believed to be true; and further that these statements were made with the knowledge that willful false statements and the like so made are punishable by fine or imprisonment or both, under 18 U.S.C. § 1001 and that such willful false statements may jeopardize the validity of the application or any patent issued thereon.

Full name of sole or first inventor DEBORAH KNUTZON

Inventor's signature _____

Date _____

Residence 6110 Rockhurst Way, Granite Bay, California 95746

Citizenship U.S.A.

Post Office Address 6110 Rockhurst Way, Granite Bay, California 95746

Full name of second joint inventor, if any, PRADIP MUKERJI

Inventor's signature _____

Date _____

Residence 1069 Arcaro Drive, Gahanna, Ohio 43230

Citizenship Republic of China, Canada

Post Office Address 1069 Arcaro Drive, Gahanna, Ohio 43230

Full name of third joint inventor, if any, YUNG-SHENG HUANG

Inventor's signature _____

Date _____

Residence 2462 Danvers Court, Upper Arlington, Ohio 43220

Citizenship U.S.A.

Post Office Address 2462 Danvers Court, Upper Arlington, Ohio 43220

Full name of fourth joint inventor, if any, JENNIFER THURMOND

Inventor's signature _____

Date _____

Residence 3702 Adirondack, Columbus, Ohio 43231

Citizenship U.S.A.

Post Office Address 3702 Adirondack, Columbus, Ohio 43231

5-00
Full name of fifth joint inventor, if any, SUNITA CHAUDHARY

Inventor's signature S Chaudhary

Date 8/6/98

Residence 3419 Woodbine Place, Pearland, Texas 77584

Citizenship India

Post Office Address 3419 Woodbine Place, Pearland, Texas 77584

Full name of sixth joint inventor, if any, AMANDA EUN-YEONG LEONARD

Inventor's signature _____

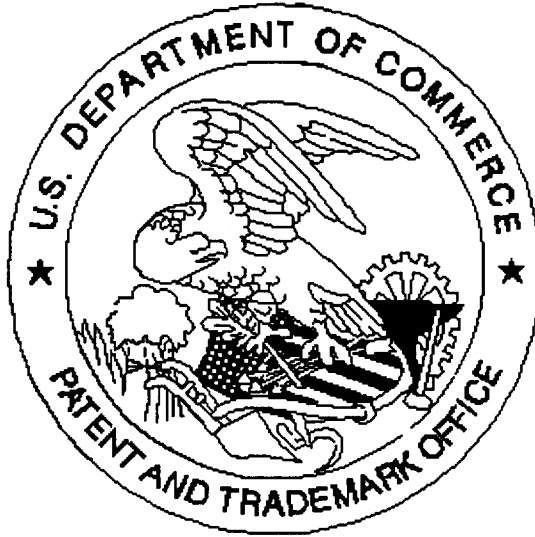
Date _____

Residence 581 Shadewood Court, Gahanna, Ohio 43230

Citizenship U.S.A.

Post Office Address 581 Shadewood Court, Gahanna, Ohio 43230

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